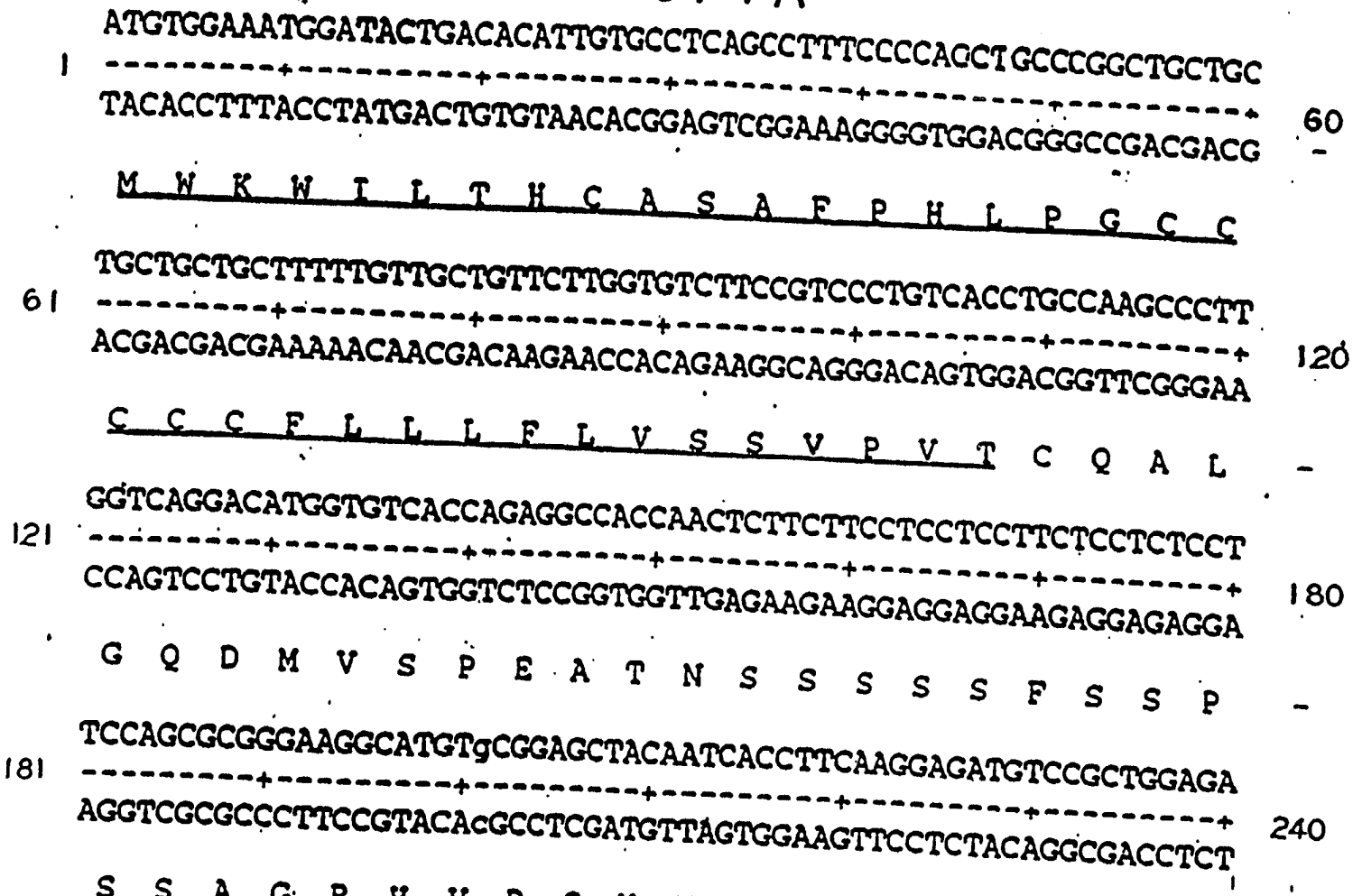
FIG. 1A



MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

FIG. 1B

```
                AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG
241             ---------+---------+---------+---------+---------+---------+ 300
                TTCGATAAGAGAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC

                 K  L  F  S  F  T  K  Y  F  L  K  I  E  K  N  G  K  V  S  G  -

                ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT
301             ---------+---------+---------+---------+---------+---------+ 360
                TGGTTCTTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA

                 T  K  K  E  N  C  P  Y  S  I  L  E  I  T  S  V  E  I  G  V  -

                GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC
361             ---------+---------+---------+---------+---------+---------+ 420
                CAACGGCAGTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG

                 V  A  V  K  A  I  N  S  N  Y  Y  L  A  M  N  K  K  G  K  L  -

                TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA
421             ---------+---------+---------+---------+---------+---------+ 480
                ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT

                 Y  G  S  K  E  F  N  N  D  C  K  L  K  E  R  I  E  E  N  G  -
```

MATCH WITH FIG. 1C

MATCH WITH FIG. 1B

FIG. 1C

```
     TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG
481  ---------+---------+---------+---------+---------+---------+ 540
     ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC

      Y  N  T  Y  A  S  F  N  W  Q  H  N  G  R  Q  M  Y  V  A  L  -

     AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC
541  ---------+---------+---------+---------+---------+---------+ 600
     TTACCTTTTCCTCGAGGTTCCTCTCCTGTCTTTTGTGCTTCCTTTTTGTGGAGACGAGTG

      N  G  K  G  A  P  R  R  G  Q  K  T  R  R  K  N  T  S  A  H  -

     TTTCTTCCAATGGTGGTACACTCATAG
601  ---------+---------+------- 627
     AAAGAAGGTTACCACCATGTGAGTATC
      F  L  P  M  V  V  H  S  *
```

FIG. 2A

```
      1                                                    50
FGF4  MS.GPGTAAV ALLPAVLLAL LA........ .PWAGRGGAA APTAPNGTLE
FGF6  MSRGAGRLQG TLWALVFLGI LV........ .GMVVPSPAG TR.ANNTLLD
FGF5  .......MSL SFLLLLFFSH LILSAWAHGE KRLAPKGQPG PAATDRNPIG
FGF1  .......... .......... .......... .......... ..........
FGF2  .......... .......... .......... .......... ..........
FGF9  .......... .......... .......... .......... ..........
FGF7  .......... ......MHKW ILTWILPTLL .....YRSCF HIICLVGTIS
KGF2  .......... ......MWKW ILTHCASAFP HLPGCCCCCF LLLFLVSSVP
FGF3  .......... .......... .......... .......MGL IWLLLLSLLE
FGF8  MGSPRSALSC LLLHLLVLCL QAQVRSAAQK RGPGAGNPAD TLGQGHEDRP

      51                                                  100
FGF4  AELERRWESL VALSLARLPV AA..QPKEAA VQSGAGDY.. ...LLGIKRL
FGF6  S...RGWGTL LSRSRAGLAG EI......AG VNWESG.Y.. ...LVGIKRQ
FGF5  SSSRQSSSSA MSSSSASSSP AASLGSQGSG LEQSSFQW.. ...SPSGRRT
FGF1  ......MAEG EITTFTALTE KFN...LPPG .......N.. ...YK...KP
FGF2  ......MAAG SITTLPALPE DGGSGAFPPG .......H.. ...FK...DP
FGF9  FGNVPVLPVD SPVLLSDHLG QSEAGGLPRG PAVTDLDH.. ...LKGILRR
FGF7  LACNDMTPEQ M...ATNVNC ......SSPE RHTRSYDY.. ...MEGGDIR
KGF2  VTCQALGQDM VSPEATNSSS SSFSSPSSAG RHVRSYNH.. ...LQ.GDVR
FGF3  PGWPAAGPGA .......... ...RLRRDAG GRGGVYEH.. ...L.GGAPR
FGF8  FGQRSRAGKN FTNPAPNYPE EGSKEQRDSV LPKVTQRHVR EQSLVTDQLS
```

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

FIG. 2B

	101				150
FGF4	RRL.....YC	NVGIGFHLQA	LPDGRIGGAH	ADT.RDSLLE	LSPVERGV.V
FGF6	RRL.....YC	NVGIGFHLQV	LPDGRISGTH	EEN.PYSLLE	ISTVERGV.V
FGF5	GSL.....YC	RVGIGFHLQI	YPDGKVNGSH	EAN.MLSVLE	IFAVSQGI.V
FGF1	KLL.....YC	SNG.GHFLRI	LPDGTVDGTR	DRSDQHIQLQ	LSAESVGE.V
FGF2	KRL.....YC	KNG.GFFLRI	HPDGRVDGVR	EKSDPHIKLQ	LQAEERGV.V
FGF9	RQL.....YC	R.T.GFHLEI	FPNGTIQGTR	KDHSRFGILE	FISIAVGL.V
FGF7	VRR.....LF	CRT.QWYLRI	DKRGKVKGTQ	EMKNNYNIME	IRTVAVGI.V
KGF2	*WRK.....LF*	*SFT.KYFLKI*	*EKNGKVSGTK*	*KENCPYSILE*	*ITSVEIGV.V*
FGF3	RRK.....LY	CAT.KYHLQL	HPSGRVNGSL	.ENSAYSILE	ITAVEVGI.V
FGF8	RRLIRTYQLY	SRTSGKHVQV	LANKRINAMA	EDGDPFAKLI	VETDTFGSRV

	151				200
FGF4	SIFGVASRFF	VAMSSKGKLY	G.SPFFTDEC	TFKEILLPNN	YNAYESYKYP
FGF6	SLFGVRSALF	VAMNSKGRLY	A.TPSFQEEC	KFRETLLPNN	YNAYESDLYQ
FGF5	GIRGVFSNKF	LAMSKKGKLH	A.SAKFTDDC	KFRERFQENS	YNTYASAIHR
FGF1	YIKSTETGQY	LAMDTDGLLY	G.SQTPNEEC	LFLERLEENH	YNTYISKKH.
FGF2	SIKGVCANRY	LAMKEDGRLL	A.SKCVTDEC	FFFERLESNN	YNTYRSRKY.
FGF9	SIRGVDSGLY	LGMNEKGELY	G.SEKLTQEC	VFREQFEENW	YNTYSSNLYK
FGF7	AIKGVESEFY	LAMNKEGKLY	A.KKECNEDC	NFKELILENH	YNTYAS....
KGF2	*AVKAINSNYY*	*LAMNKKGKLY*	*G.SKEFNNDC*	*KLKERIEENG*	*YNTYAS....*
FGF3	AIRGLFSGRY	LAMNKRGRLY	A.SEHYSAEC	EFVERIHELG	YNTYASRLYR
FGF8	RVRGAETGLY	ICMNKKGKLI	AKSNGKGKDC	VFTEIVLENN	YTALQNAKY.

MATCH WITH FIG. 2C

MATCH WITH FIG. 2B

FIG. 2C

```
      201                                                      250
FGF4  .......... GM......FI ALSKNGKTKK G..NRVSPTM KVTHFLPRL.
FGF6  .......... GT......YI ALSKYGRVKR G..SKVSPIM TVTHFLPRI.
FGF5  .......... TEKTGREWYV ALNKRGKAKR GCSPRVKPQH ISTHFLPRFK
FGF1  .......... ...AEKNWFV GLKKNGSCKR G..PRTHYGQ KAILFLPLPV
FGF2  .......... ...T..SWYV ALKRTGQYKL G..SKTGPGQ KAILFLPMSA
FGF9  HV........ ..DTGRRYYV ALNKDGTPRE G..TRTKRHQ KFTHFLPRPV
FGF7  .......AKW THNGGEM.FV ALNQKGIPVR G..KKTKKEQ KTAHFLPMAI
KGF2  .......FNW QHNGRQM.YV ALNGKGAPRR G..QKTRRKN TSAHFLPMVV
FGF3  TVSSTPGARR QPSAERLWYV SVNGKGRPRR G..FKTRRTQ KSSLFLPRVL
FGF8  .......... .....EGWYM AFTRKGRPRK G..SKTRQHQ REVHFMKRLP

      251                                                      300
FGF4  .......... .......... .......... .......... ..........
FGF6  .......... .......... .......... .......... ..........
FGF5  QSEQPELSFT VTVPEKKNPP SPIKSKIPLS APRKNTNSVK YRLKFRFG..
FGF1  SSD....... .......... .......... .......... ..........
FGF2  KS........ .......... .......... .......... ..........
FGF9  DPDKVPELYK DILSQS.... .......... .......... ..........
FGF7  T......... .......... .......... .......... ..........
KGF2  HS........ .......... .......... .......... ..........
FGF3  DHRDHEMVRQ LQSGLPRPPG KGVQPRRRRQ KQSPDNLEPS HVQASRLGSQ
FGF8  RGHHTTEQSL RFEFLNYPPF TRSLRGSQRT WAPEPR.... ..........
```

MATCH WITH FIG. 2D

FIG. 2D

MATCH WITH FIG. 2C

	301
FGF4	......
FGF6	......
FGF5	......
FGF1	......
FGF2	......
FGF9	......
FGF7	......
KGF2	......
FGF3	LEASAH
FGF8	......

Figure 3A

```
GGAATTCCGG GAAGAGAGGG AAGAAAACAA CGGCGACTGG GCAGCTGCCT CCACTTCTGA      60

CAACTCCAAA GGGATATACT TGTAGAAGTG GCTCGCAGGC TGGGGCTCCG CAGAGAGAGA     120

CCAGAAGGTG CCAACCGCAG AGGGGTGCAG ATATCTCCCC CTATTCCCCA CCCCACCTCC     180

CTTGGGTTTT GTTCACCGTG CTGTCATCTG TTTTTCAGAC CTTTTTGGCA TCTAACATGG     240

TGAAGAAAGG AGTAAAGAAG AGAACAAAGT AACTCCTGGG GGAGCGAAGA GCGCTGGTGA     300

CCAACACCAC CAACGCCACC ACCAGCTCCT GCTGCTGCGG CCACCCACGT CCACCATTTA     360

CCGGGAGGCT CCAGAGGCGT AGGCAGCGGA TCCGAGAAAG GAGCGAGGGG AGTCAGCCGG     420

CTTTTCCGAG GAGTTATGGA TGTTGGTGCA TTCACTTCTG GCCAGATCCG CGCCCAGAGG     480

GAGCTAACCA GCAGCCACCA CCTCGAGCTC TCTCCTTGCC TTGCATCGGG TCTTACCCTT     540

CCAGTATGTT CCTTCTGATG AGACAATTTC CAGTGCCGAG AGTTTCAGTA CA ATG          595
                                                              Met

TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG CCC       643
Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro

GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC GTC       691
Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val

CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG GCC       739
Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala

ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA AGG       787
Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg

CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA AAG       835
His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys

CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG AAG       883
Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys

GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA       931
Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile

ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC       979
Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn

TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA      1027
Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu

TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC      1075
Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr
```

Figure 3B

```
AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT -    1123
Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr

GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA    1171
Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg

AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA        1216
Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser

TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG  1276

GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC  1336

TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCACTG CTGACATATG ATGTTCTTTT  1396

AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT  1456

ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTTGTTGT TGTTGTCAAG TTTTTGTTTT  1516

TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG  1576

GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT  1636

GAATCAATGA ACAGTAATAC GTGCAAGCAT TTACTGGAAA GCACTTGGGT CATATCATAT  1696

GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA  1756

TAAACATGTT AGTGTGAAAC TGTTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC  1816

TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT  1876

TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG  1936

CACACCACAT GCATGTTCAC GACAAAGTGT TTTTAAAACT TGGCGAACAC TTCAAAAATA  1996

GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA  2056

CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG  2116

AGATGTCTGC TATCATTTGA AAACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA  2176

GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA  2236

AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT  2296

TTCTTGCCAA ATGTCATGGC GGTAAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA  2356

TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT  2416
```

Figure 3C

```
CCCAGGGGCT TAAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA   2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAAACCAA ATAAAACTTG TTTTCTGTAA   2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC   2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT   2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT   2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT   2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGGACA CAGTATTTTG GTACAAAAAA   2836
AAAGACTCAC TAAATGTGTC TTACTAAAGT TTAACCTTTG GAAATGCTGG CGTTCTGTGA   2896
TTCTCCAACA AACTTATTTG TGTCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT   2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTTCCC   3016
ATTCTTCAAA AAAACTGTAT TTCAGAAGAA ACACATTTGA GGCACTGTCT TTTGGCTTAT   3076
AGTTTAAATT GCATTTCATC ATACTTTGCT TCCAACTTGC TTTTTGGCAA ATGAGATTAT   3136
AAAAATGTTT AATTTTTGTG GTTGGAATCT GGATGTTAAA ATTTAATTGG TAACTCAGTC   3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAACTAGGTA TCTTTTTTTC CTTTATGTTG   3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG   3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT   3376
TATTTCACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG   3436
TACTCAAGAC ACTAAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT   3496
AGAAAACATC TCCCCTGTCT CTCCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG   3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG   3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA   3676
AAACAAAACA AATGTAGCCA TGCGTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG   3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT   3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA   3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA   3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA   3976
GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA   4036
```

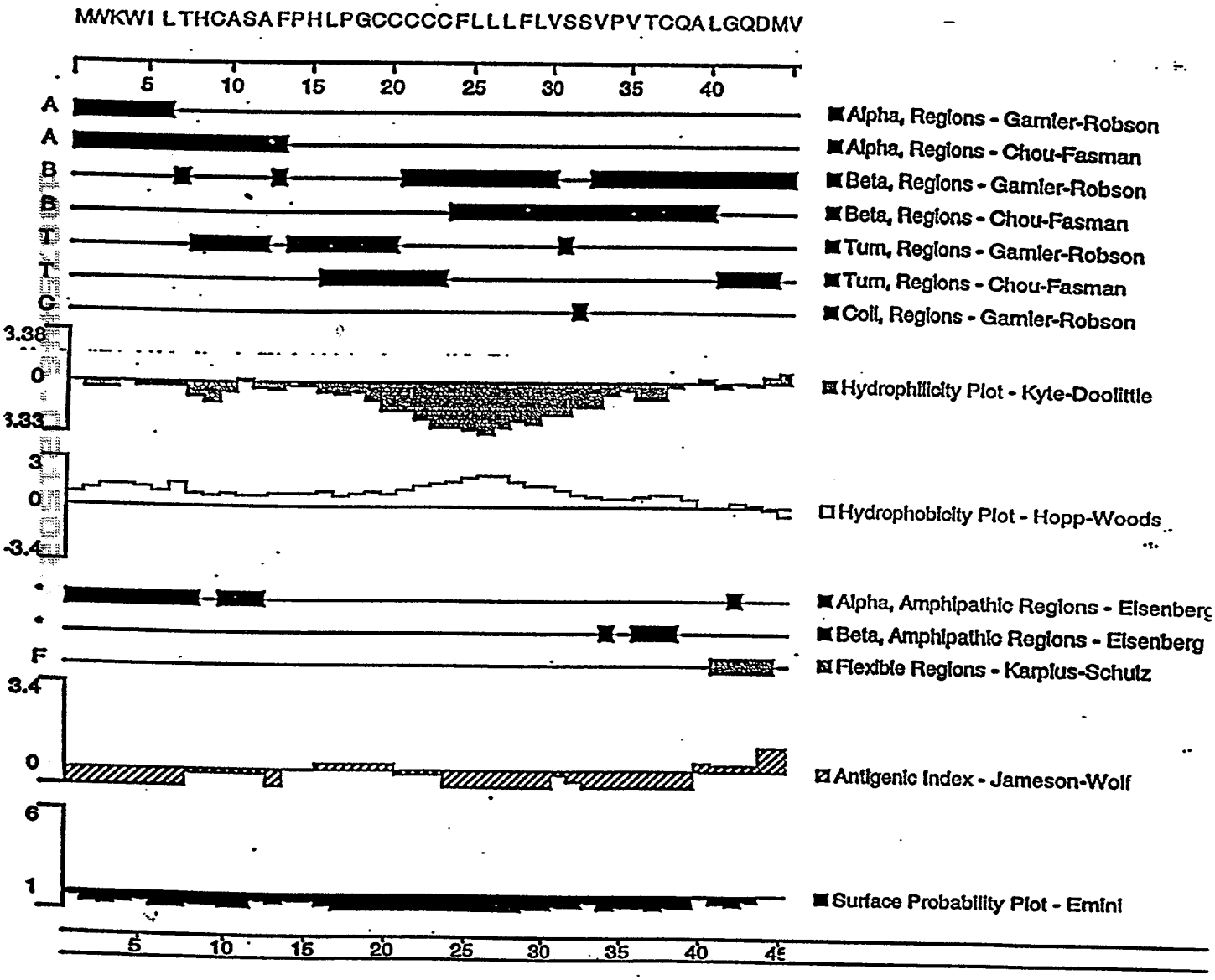
Figure 3D

ATGGAAATAG AATTCTGGTC CCTTTTGCAA CTACTGAAGA AAAAAAAAAG CAGTTTCAGC 4096

CCTGAATGTT GTAGATTTGA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA 4156

TTCGCCCTAT AGTGAGTCGT A 4177

Figure 4A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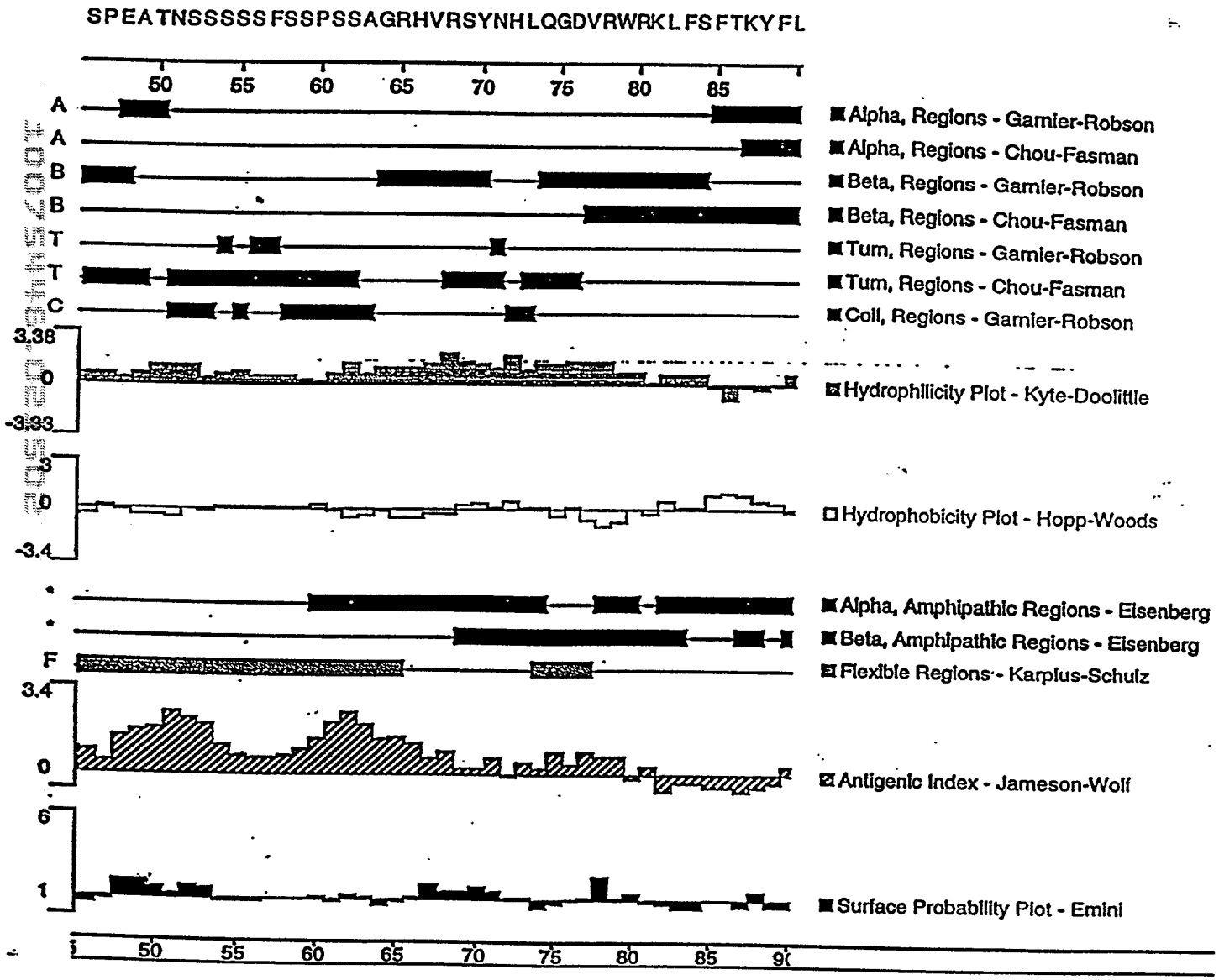
10
15
20
25
30
35
40
A
A
B
B
T
T
C
Alpha, Regions - Gamier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Gamier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Gamier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Gamier-Robson
3.38
0
-3.33
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
5
10
15
20
25
30
35
40

Figure 4B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55
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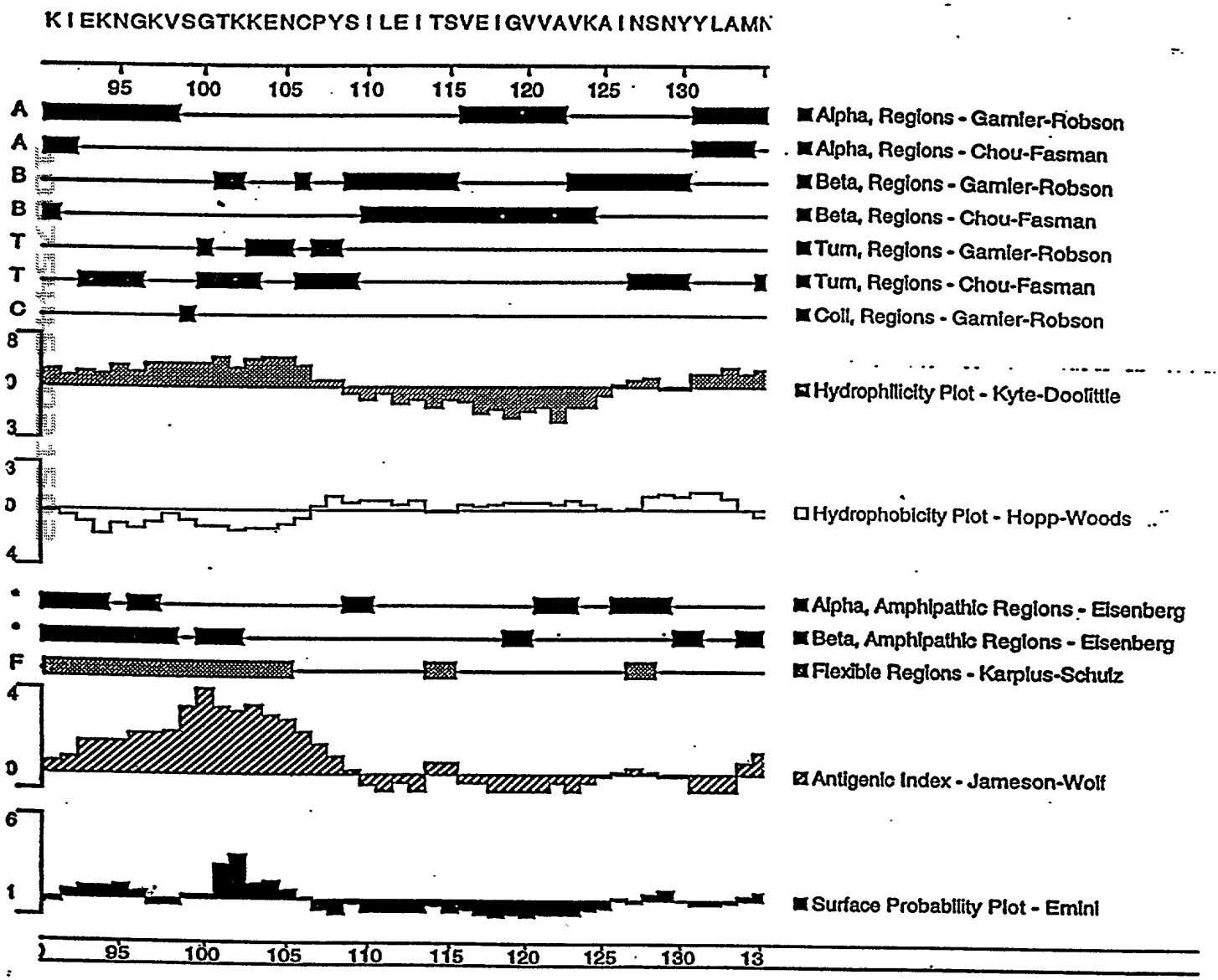
65
70
75
80
85
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
3.38
0
-3.33
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
50
55
60
65
70
75
80
85

Figure 4C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120
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A
A
B
B
T
T
C
Alpha, Regions - Gamier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Gamier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Gamier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Gamier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini
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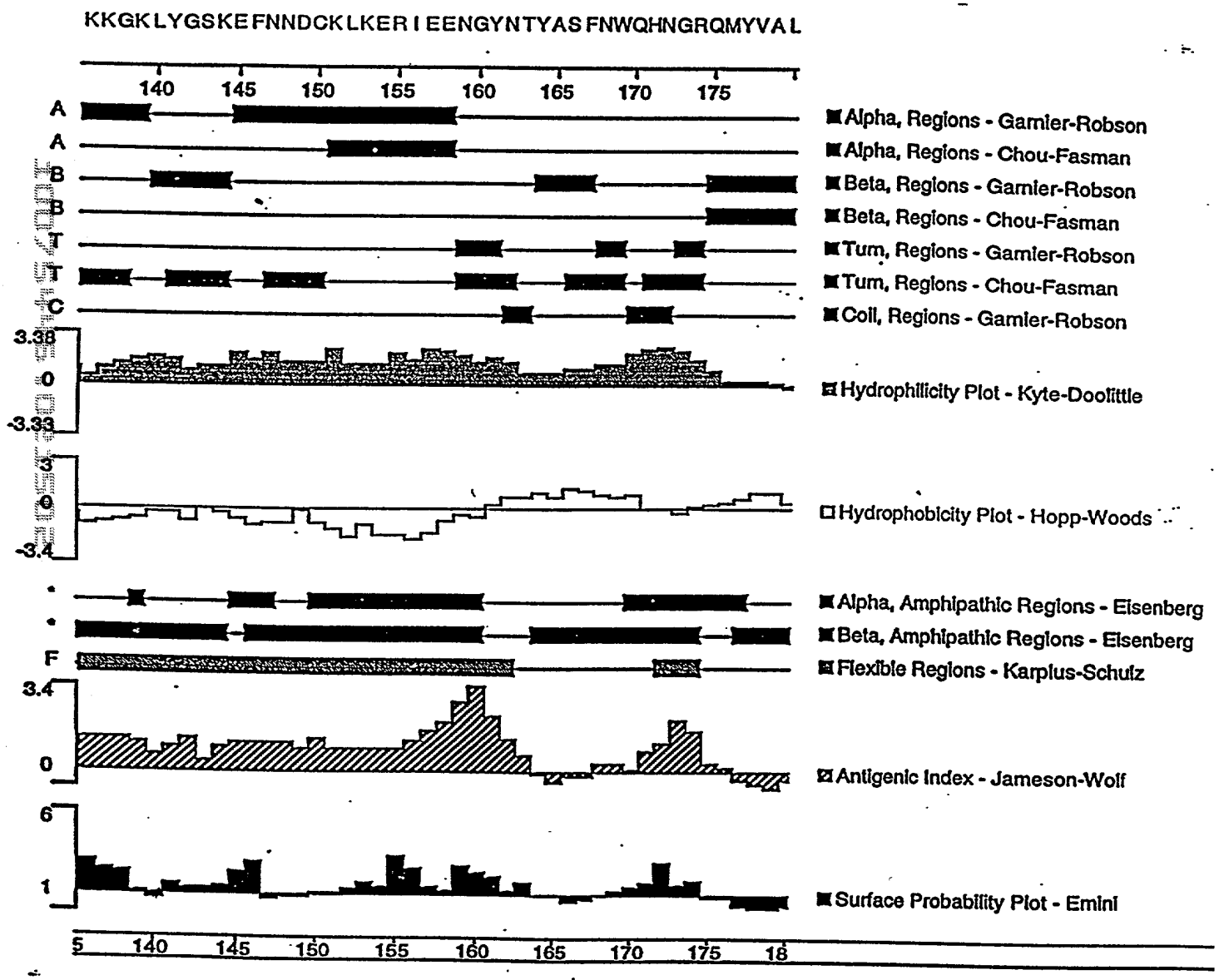
100
105
110
115
120
125
130

Figure 4D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145
150
155
160
165
170
175
A
A
B
B
T
T
C
Alpha, Regions - Gamier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Gamier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Gamier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Gamier-Robson
3.38
0
-3.33
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
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1
Surface Probability Plot - Emini
5
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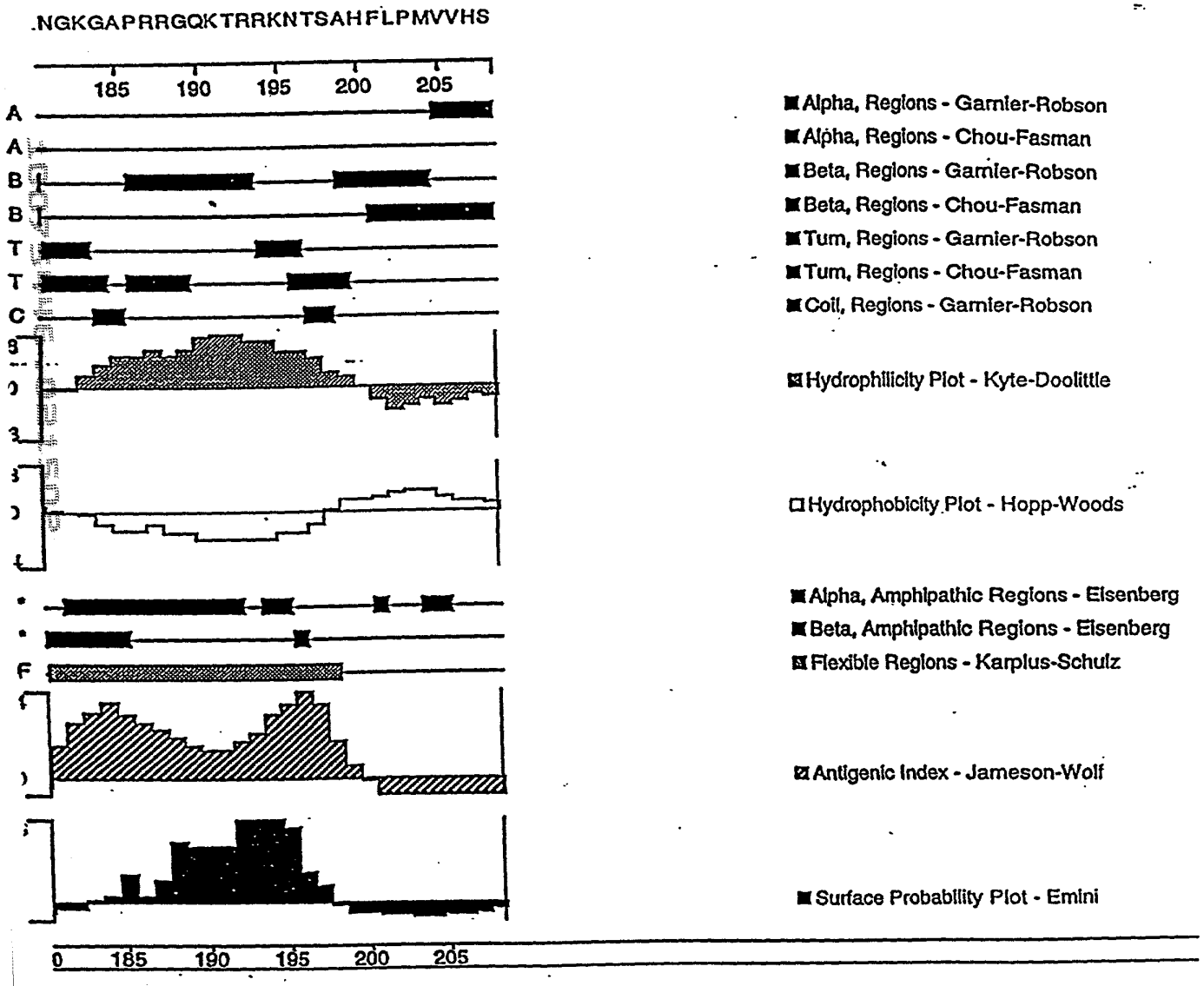
145
150
155
160
165
170
175
18

Figure 4E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185
190
195
200
205
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini
0
185
190
195
200
205

Figure 5

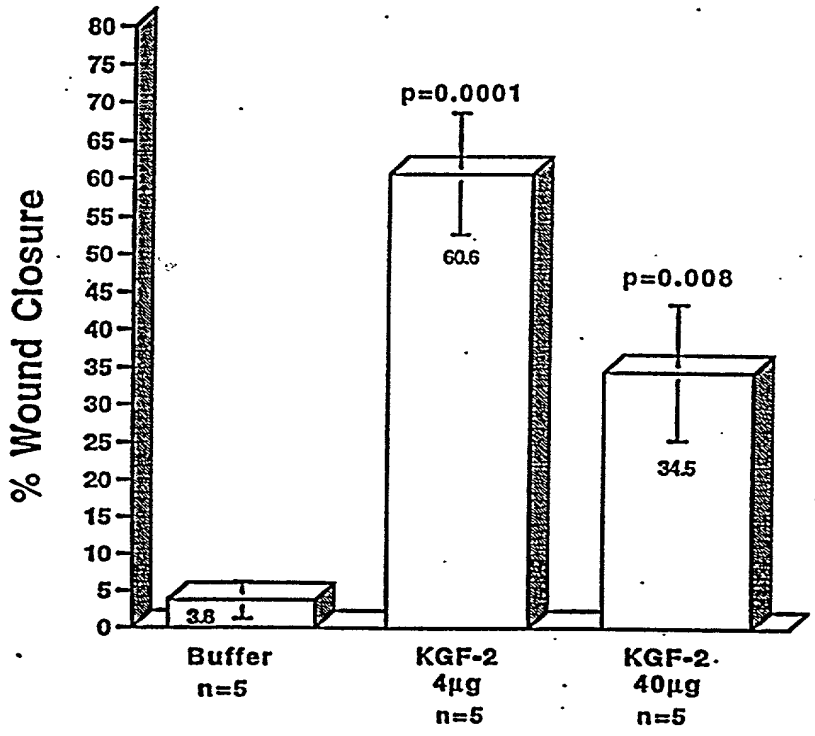

% Wound Closure
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
3.8
p=0.0001
60.6
p=0.008
34.5
Buffer
n=5
KGF-2
4µg
n=5
KGF-2
40µg
n=5

Figure 6

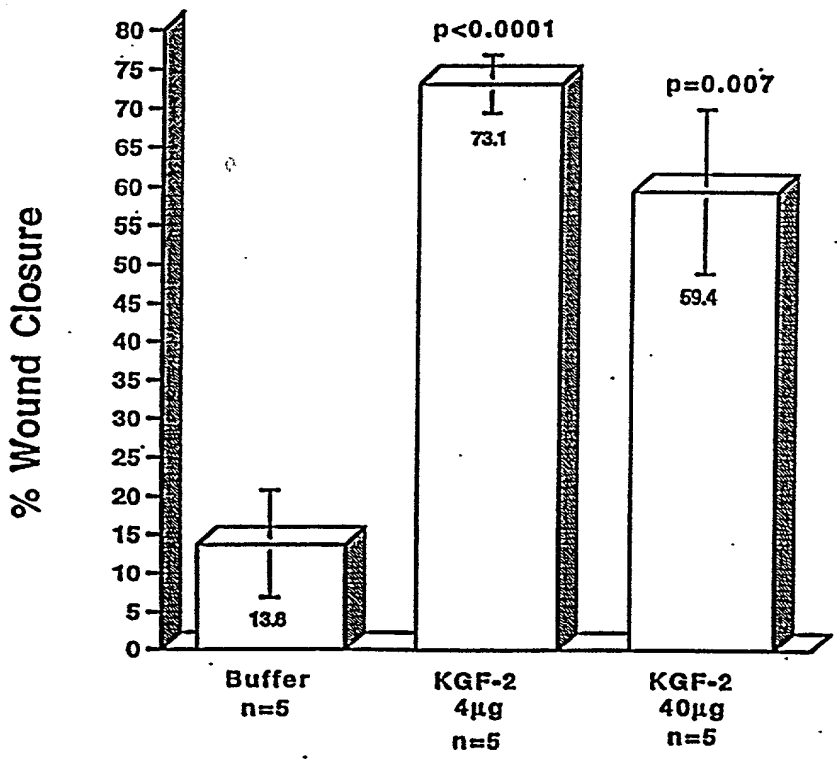

% Wound Closure
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
p<0.0001
73.1
p=0.007
59.4
13.8
Buffer
n=5
KGF-2
4µg
n=5
KGF-2
40µg
n=5

Figure 7

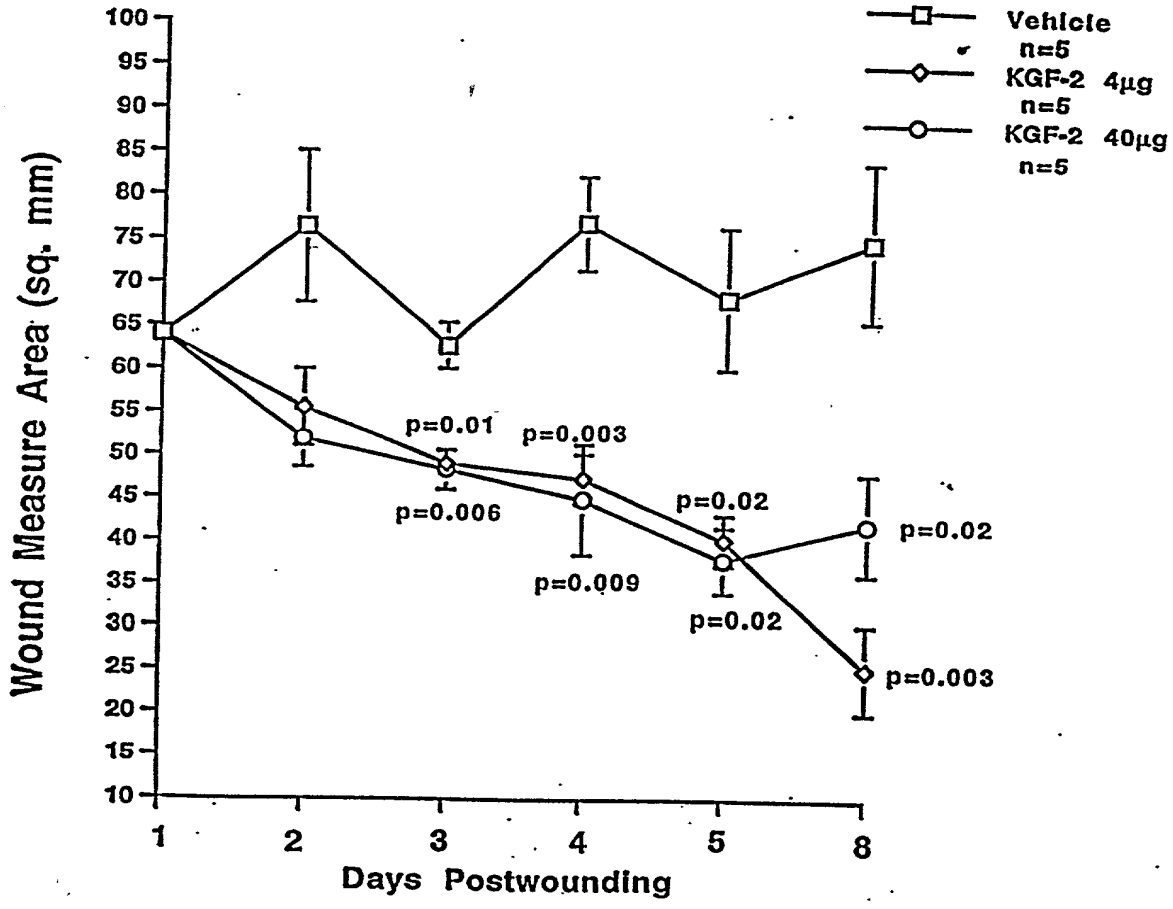

Wound Measure Area (sq. mm)
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
1
2
3
4
5
8
Days Postwounding
Vehicle
n=5
KGF-2 4µg
n=5
KGF-2 40µg
n=5
p=0.01
p=0.003
p=0.006
p=0.02
p=0.02
p=0.009
p=0.02
p=0.003

Figure 8

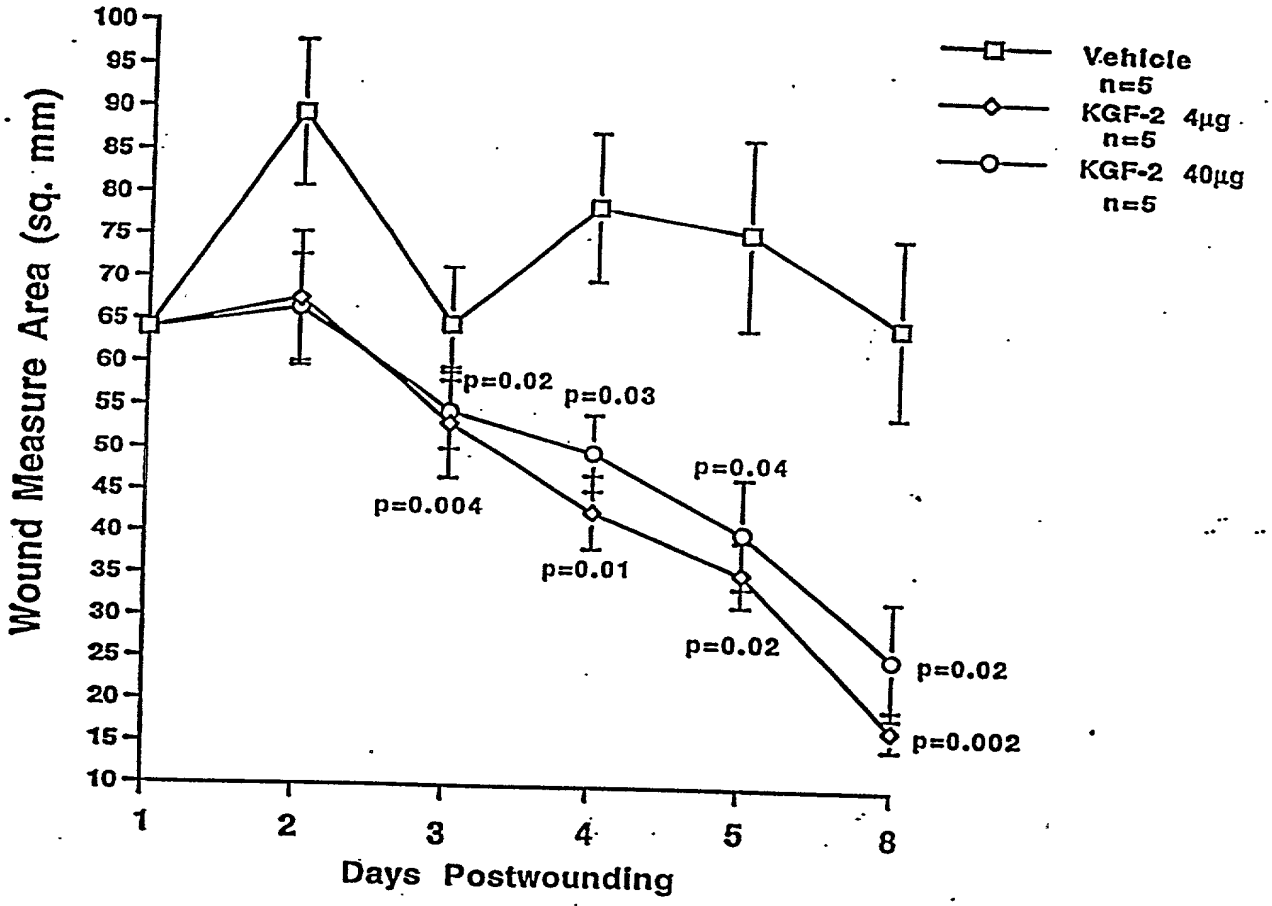
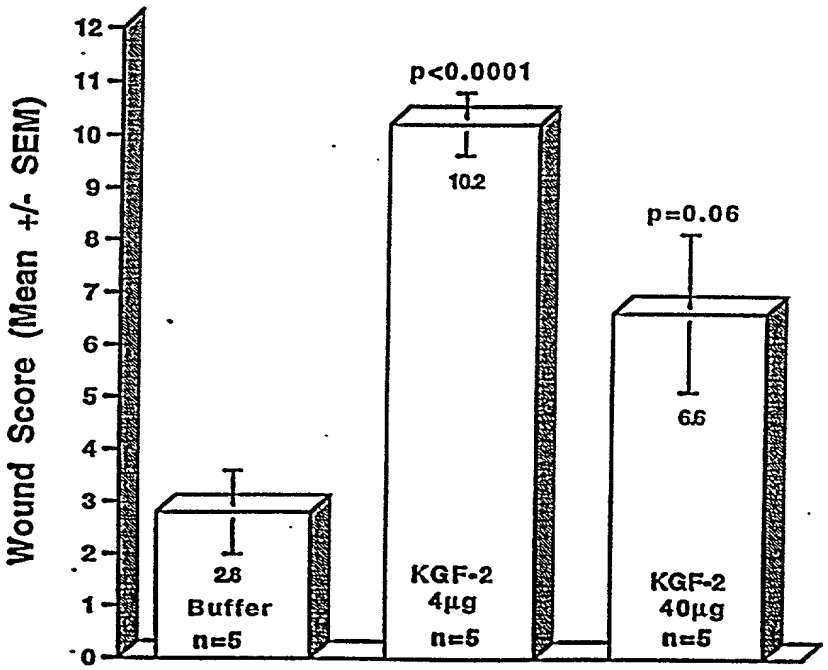
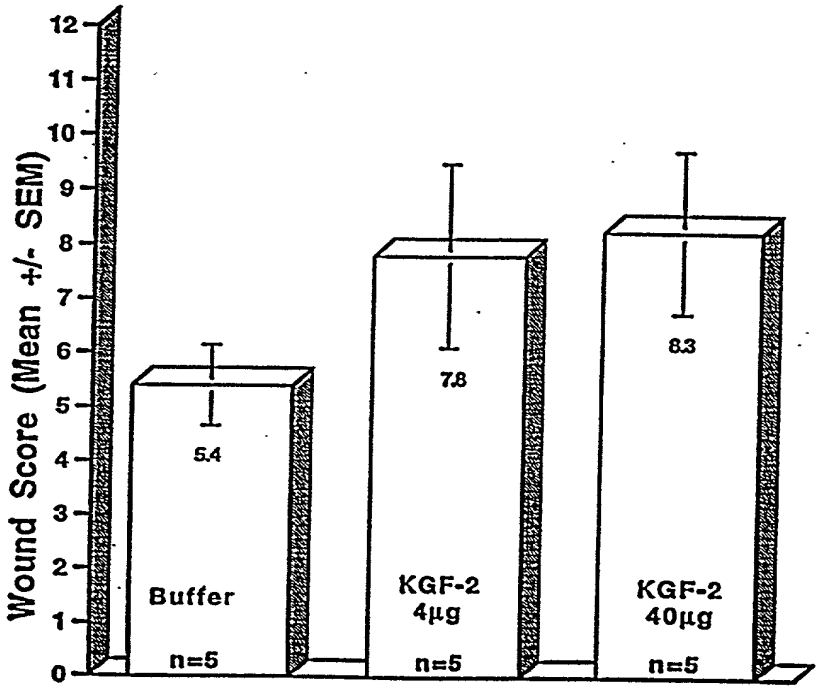

Wound Measure Area (sq. mm)
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
1
2
3
4
5
8
Days Postwounding
Vehicle
n=5
KGF-2 4µg
n=5
KGF-2 40µg
n=5
p=0.02
p=0.03
p=0.04
p=0.004
p=0.01
p=0.02
p=0.02
p=0.002

Figure 9



1-3 Minimal cell accumulation, no granulation
4-6 Immature granulation, inflammatory cells, capillaries
10-12 Fibroblasts, collagen, epithelium

Figure 10



1-3 Minimal cell accumulation, no granulation
4-6 Immature granulation, inflammatory cells, capillaries
7-9 Granulation tissue, cells, fibroblasts, new epithelium
10-12 Fibroblasts, collagen, epithelium

Figure 11

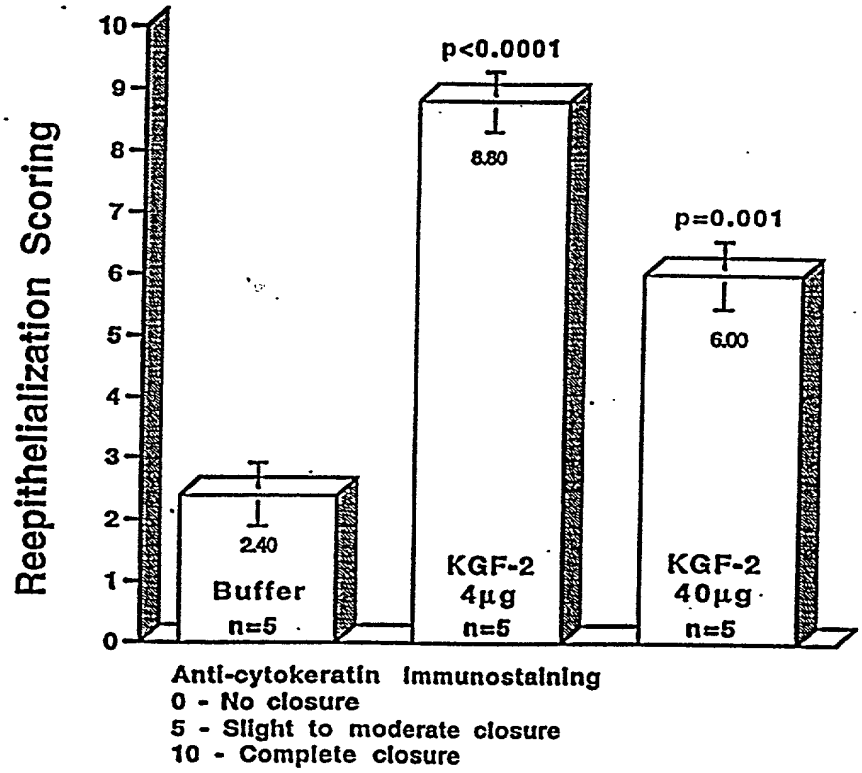

Reepithelialization Scoring
10
9
8
7
6
5
4
3
2
1
0
p<0.0001
8.80
p=0.001
6.00
2.40
Buffer
n=5
KGF-2
4µg
n=5
KGF-2
40µg
n=5
Anti-cytokeratin Immunostaining
0 - No closure
5 - Slight to moderate closure
10 - Complete closure

Figure 12

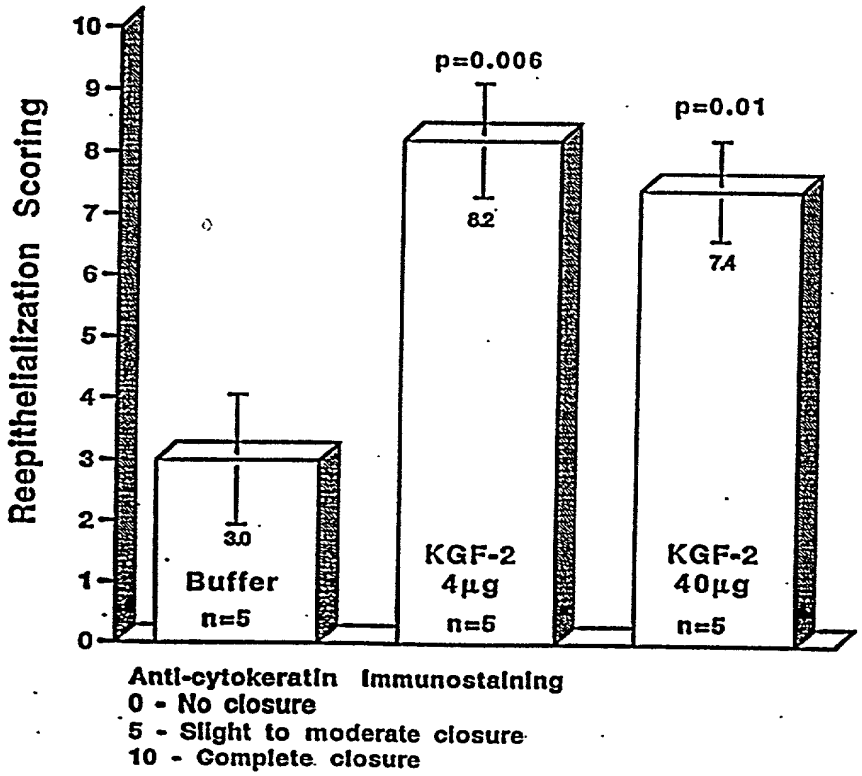

Reepithelialization Scoring
10
9
8
7
6
5
4
3
2
1
0
p=0.006
p=0.01
8.2
7.4
3.0
Buffer
n=5
KGF-2
4µg
n=5
KGF-2
40µg
n=5
Anti-cytokeratin Immunostaining
0 - No closure
5 - Slight to moderate closure
10 - Complete closure

Figure 13

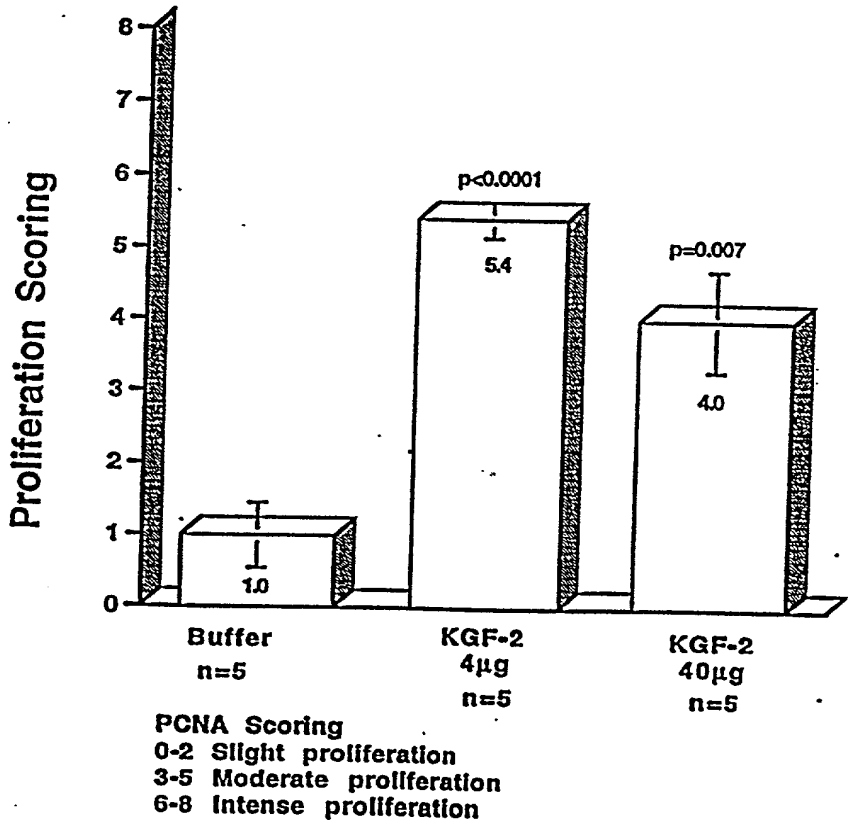
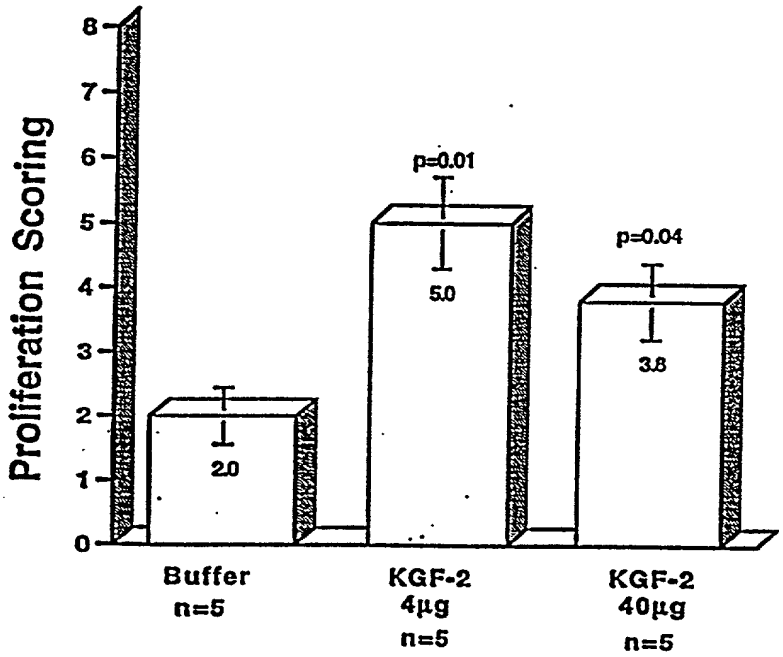

Proliferation Scoring
8
7
6
5
4
3
2
1
0
p<0.0001
5.4
p=0.007
4.0
1.0
Buffer
n=5
KGF-2
4µg
n=5
KGF-2
40µg
n=5
PCNA Scoring
0-2 Slight proliferation
3-5 Moderate proliferation
6-8 Intense proliferation

Figure 14



PCNA Scoring
0-2 Slight proliferation
3-5 Moderate proliferation
6-8 Intense proliferation

Figure 15

ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC
AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCC
CGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTC
GTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTG
GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAG
CAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAG
AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT
ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG
GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD
VRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSN
YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

kgf-2 synthetic cys37 Bam HI
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

Figure 16

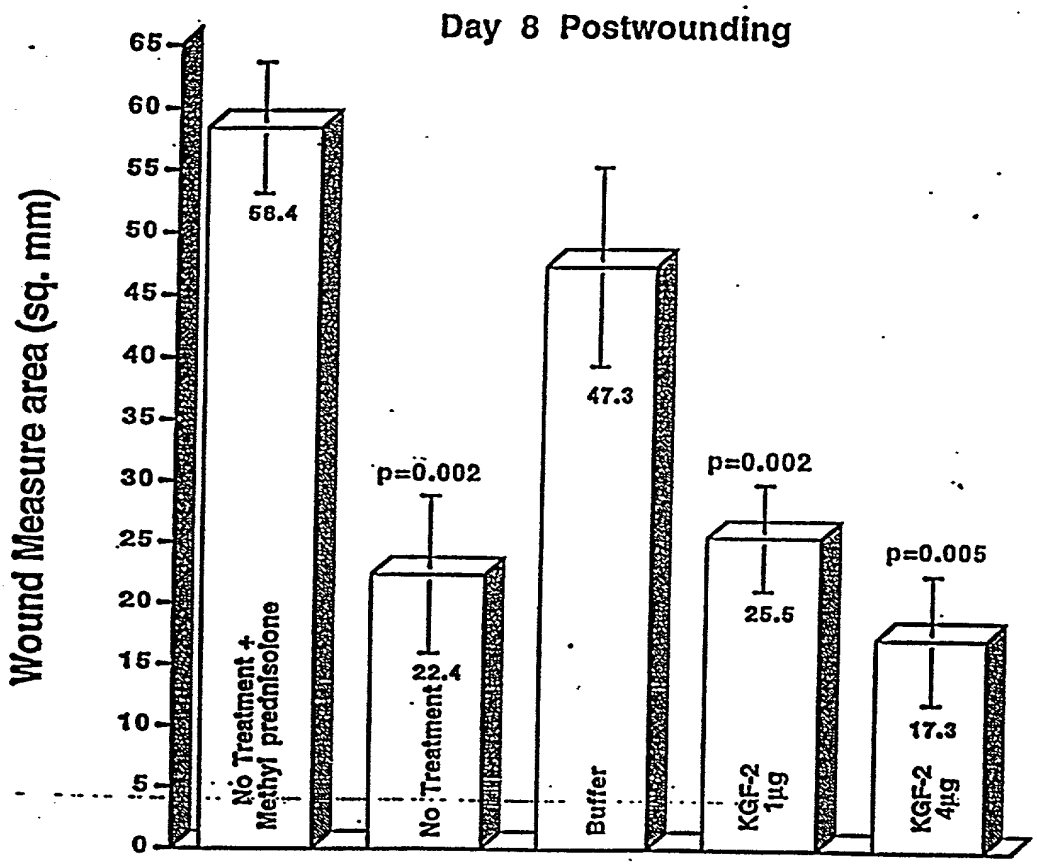

Day 8 Postwounding
Wound Measure area (sq. mm)
65
60
55
50
45
40
35
30
25
20
15
10
5
0
58.4
No Treatment + Methyl prednisolone
p=0.002
22.4
No Treatment
47.3
Buffer
p=0.002
25.5
KGF-2 1µg
p=0.005
17.3
KGF-2 4µg

Figure 17

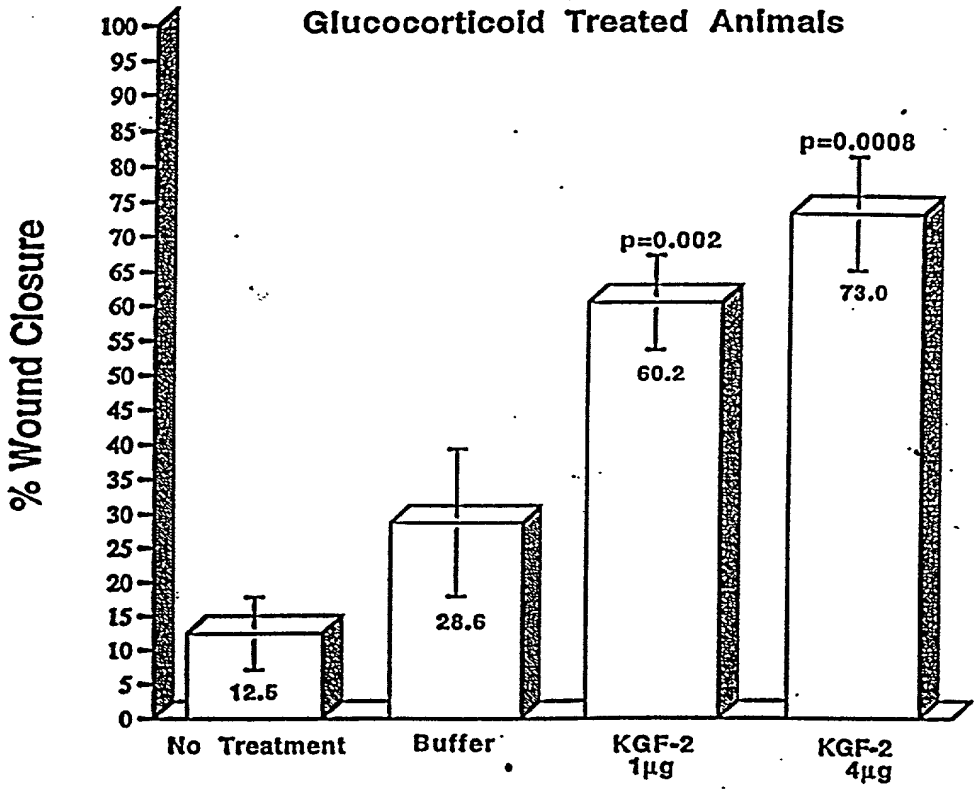

Glucocorticoid Treated Animals
% Wound Closure
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
12.5
28.6
60.2
73.0
p=0.002
p=0.0008
No Treatment
Buffer
KGF-2 1µg
KGF-2 4µg

Figure 18

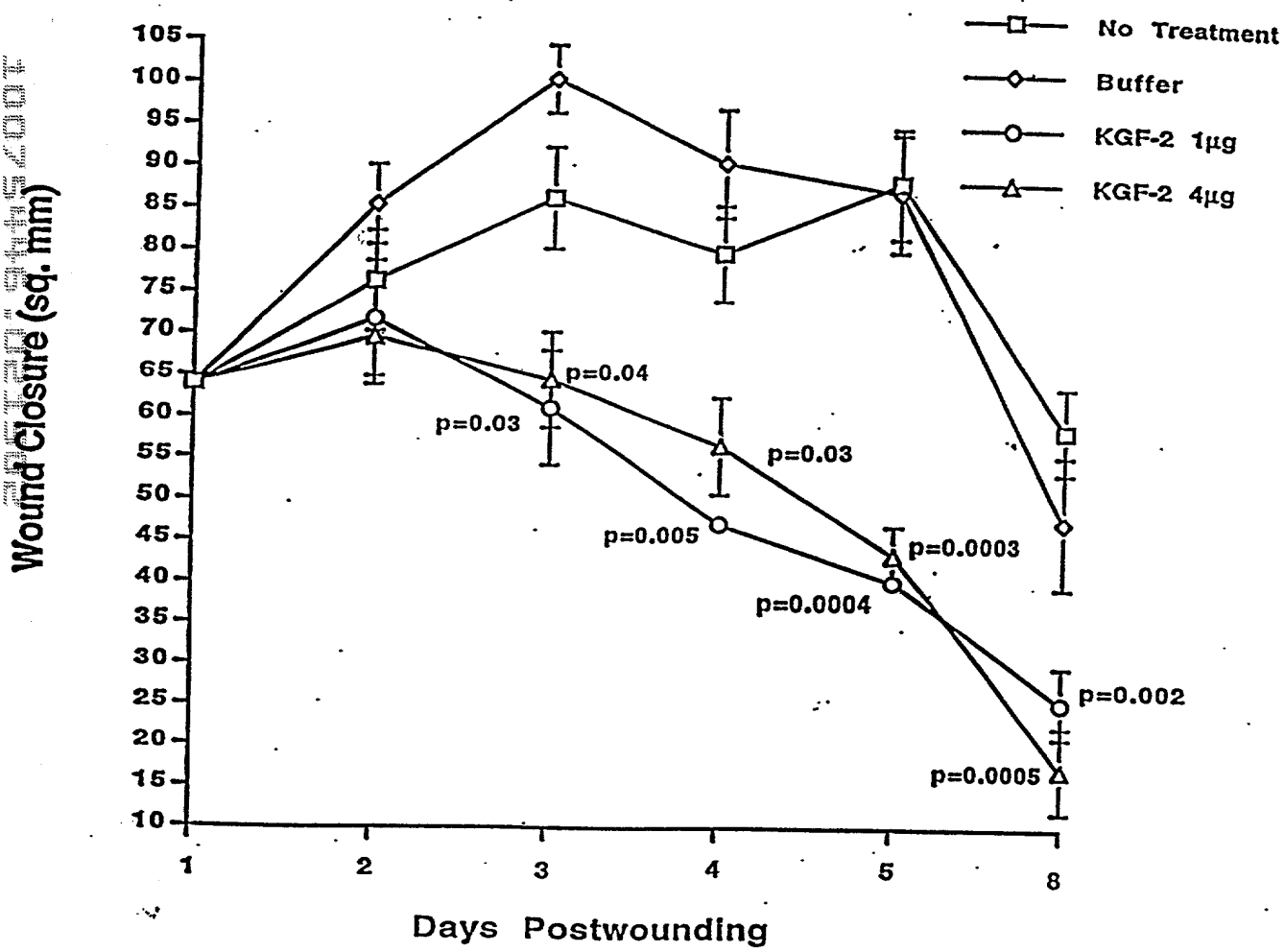

No Treatment
Buffer
KGF-2 1µg
KGF-2 4µg
Wound Closure (sq. mm)
105
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
1
2
3
4
5
8
Days Postwounding
p=0.04
p=0.03
p=0.03
p=0.005
p=0.0003
p=0.0004
p=0.002
p=0.0005

Figure 19A

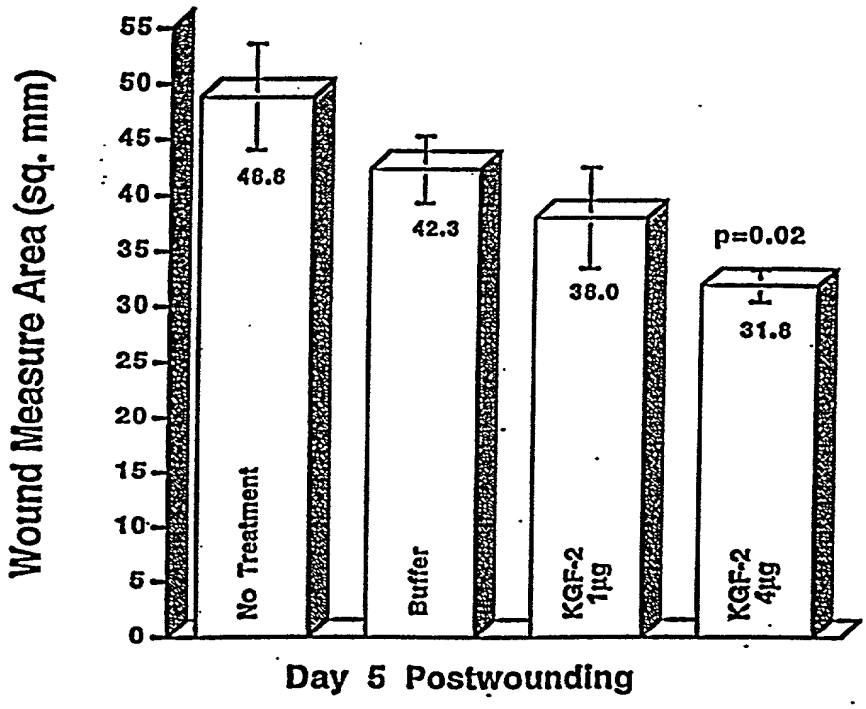

Wound Measure Area (sq. mm)
55
50
45
40
35
30
25
20
15
10
5
0
48.6
42.3
38.0
p=0.02
31.6
No Treatment
Buffer
KGF-2 1µg
KGF-2 4µg
Day 5 Postwounding

Figure 19B

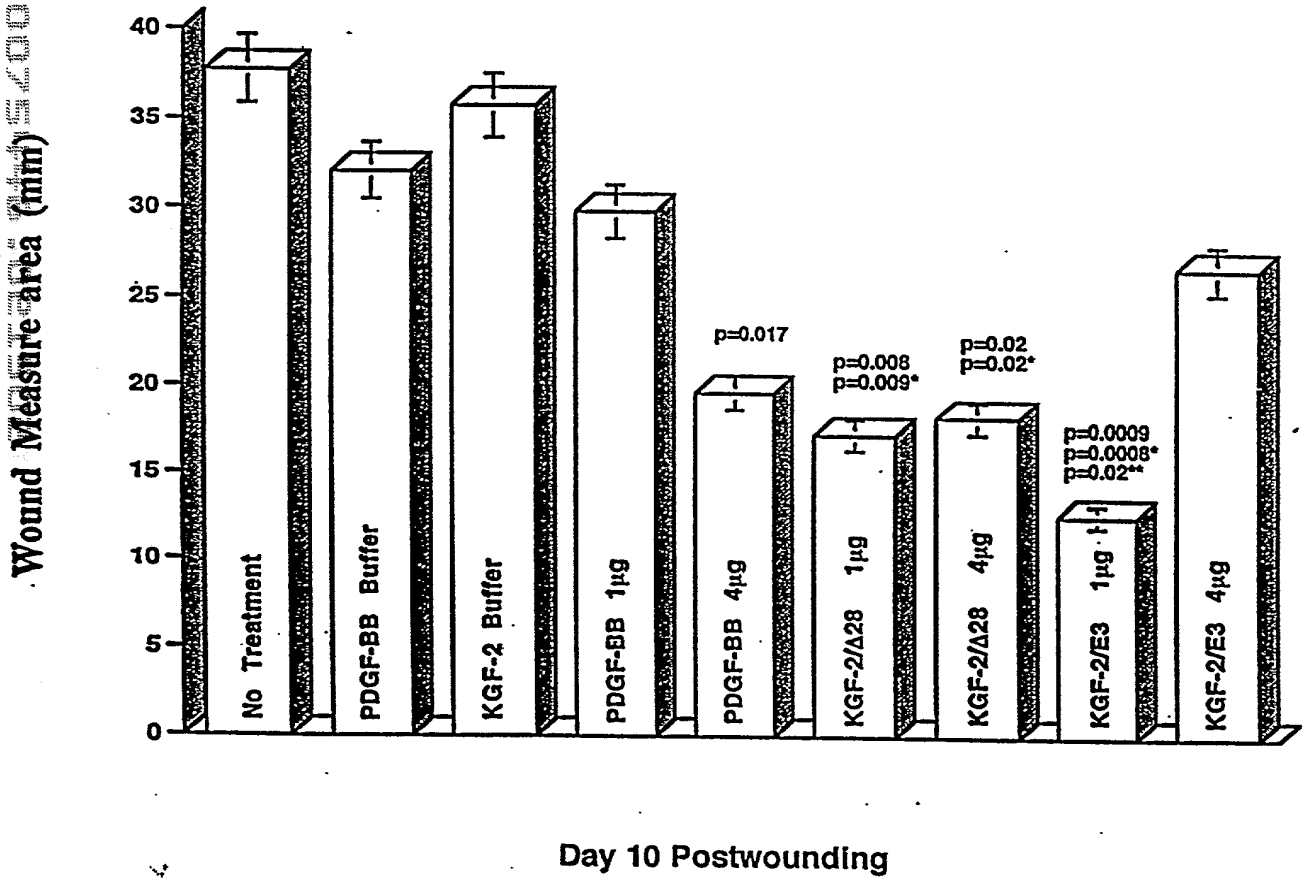

Wound Measure area (mm)
40
35
30
25
20
15
10
5
0
No Treatment
PDGF-BB Buffer
KGF-2 Buffer
PDGF-BB 1µg
PDGF-BB 4µg
KGF-2/Δ28 1µg
KGF-2/Δ28 4µg
KGF-2/E3 1µg
KGF-2/E3 4µg
p=0.017
p=0.008
p=0.009*
p=0.02
p=0.02*
p=0.0009
p=0.0008*
p=0.02**
Day 10 Postwounding

Figure 20

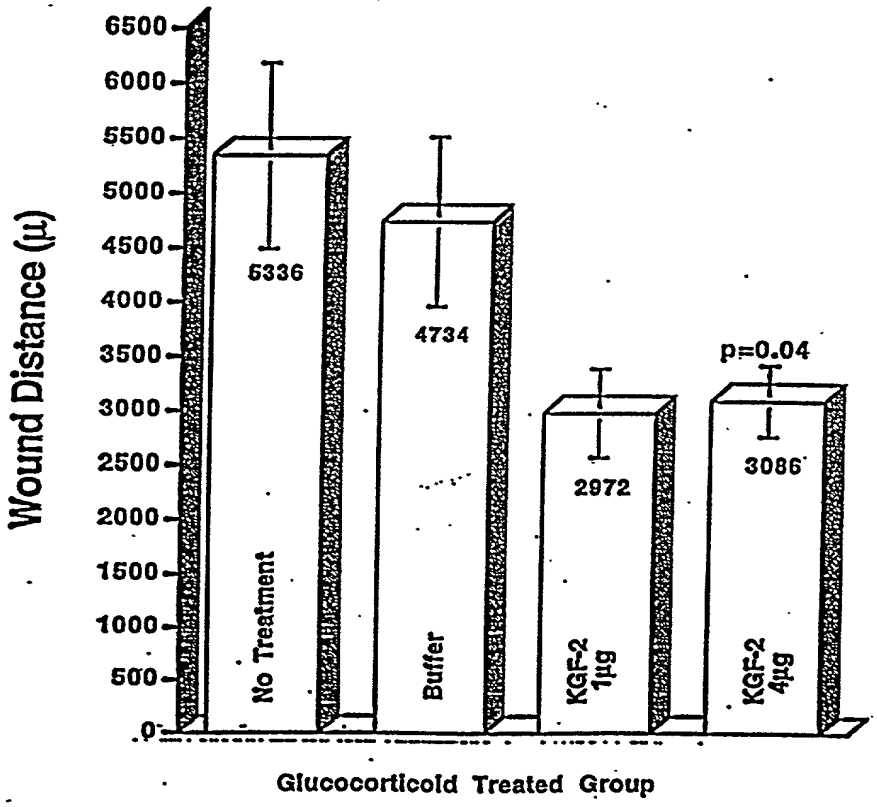

Wound Distance (μ)
6500
6000
5500
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
5336
4734
2972
3086
p=0.04
No Treatment
Buffer
KGF-2 1μg
KGF-2 4μg
Glucocorticoid Treated Group

Figure 21A

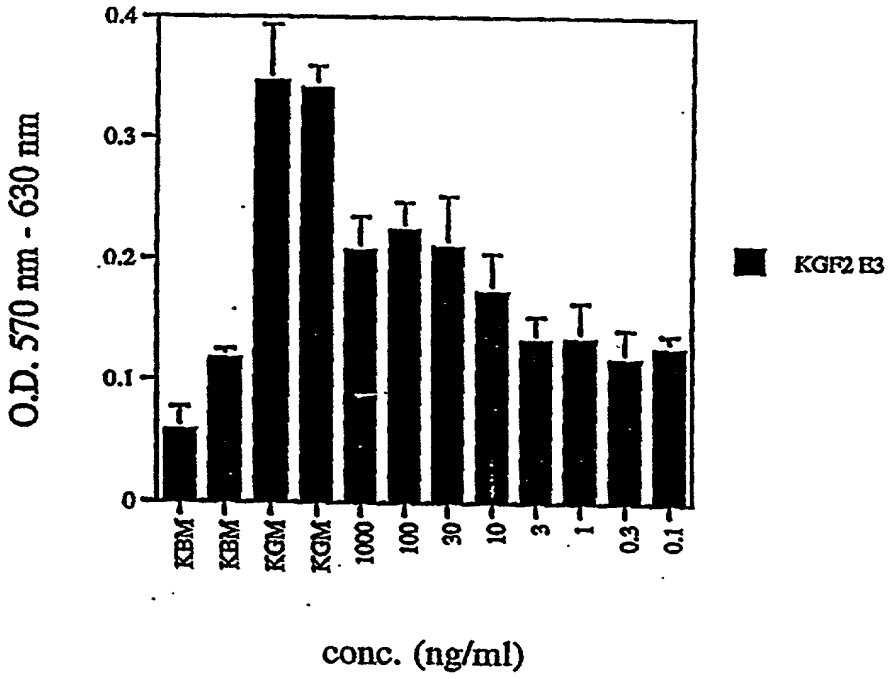

O.D. 570 nm - 630 nm
0.4
0.3
0.2
0.1
0
KBM
KBM
KGM
KGM
1000
100
30
10
3
1
0.3
0.1
conc. (ng/ml)
KGF2 E3

Figure 21B

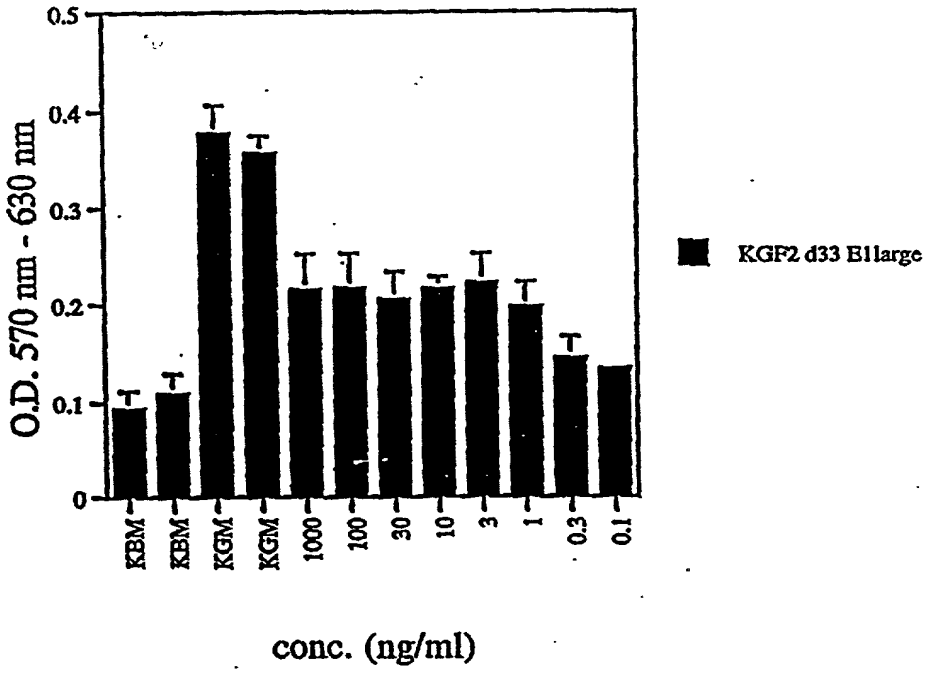

0.5
0.4
0.3
0.2
0.1
0
O.D. 570 nm - 630 nm
KBM
KBM
KGM
KGM
1000
100
30
10
3
1
0.3
0.1
conc. (ng/ml)
KGF2 d33 B1large

Figure 21C

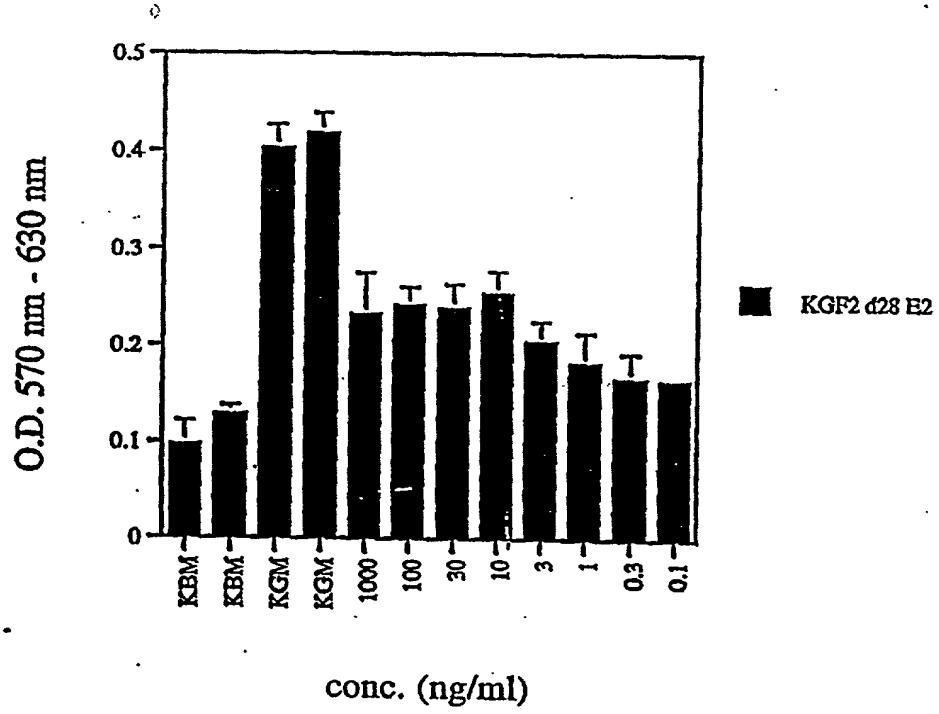

O.D. 570 nm - 630 nm
0.5
0.4
0.3
0.2
0.1
0
KBM
KBM
KGM
KGM
1000
100
30
10
3
1
0.3
0.1
conc. (ng/ml)
KGF2 d28 E2

Figure 22A

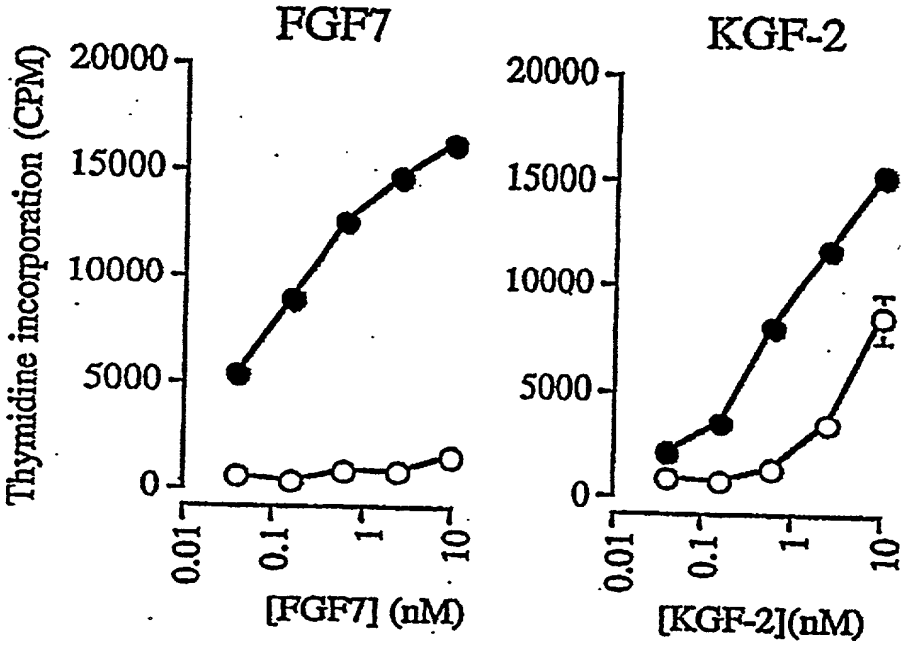

FGF7
KGF-2
Thymidine incorporation (CPM)
20000
15000
10000
5000
0
0.01
0.1
1
10
[FGF7] (nM)
[KGF-2](nM)
FGF

Figure 22B

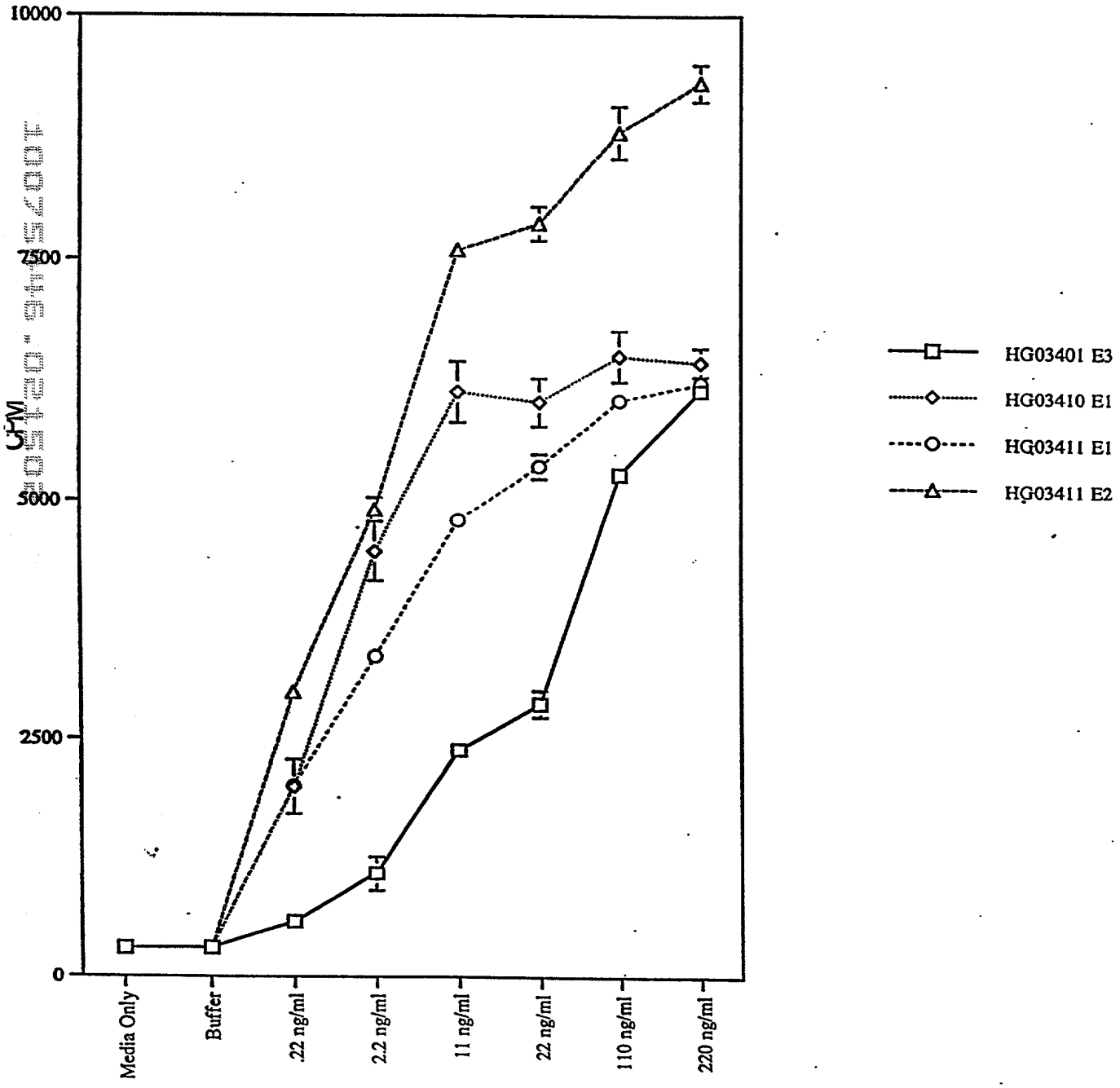

10000
7500
5000
2500
0
Media Only
Buffer
.22 ng/ml
2.2 ng/ml
11 ng/ml
22 ng/ml
110 ng/ml
220 ng/ml
HG03401 E3
HG03410 E1
HG03411 E1
HG03411 E2

Figure 22C

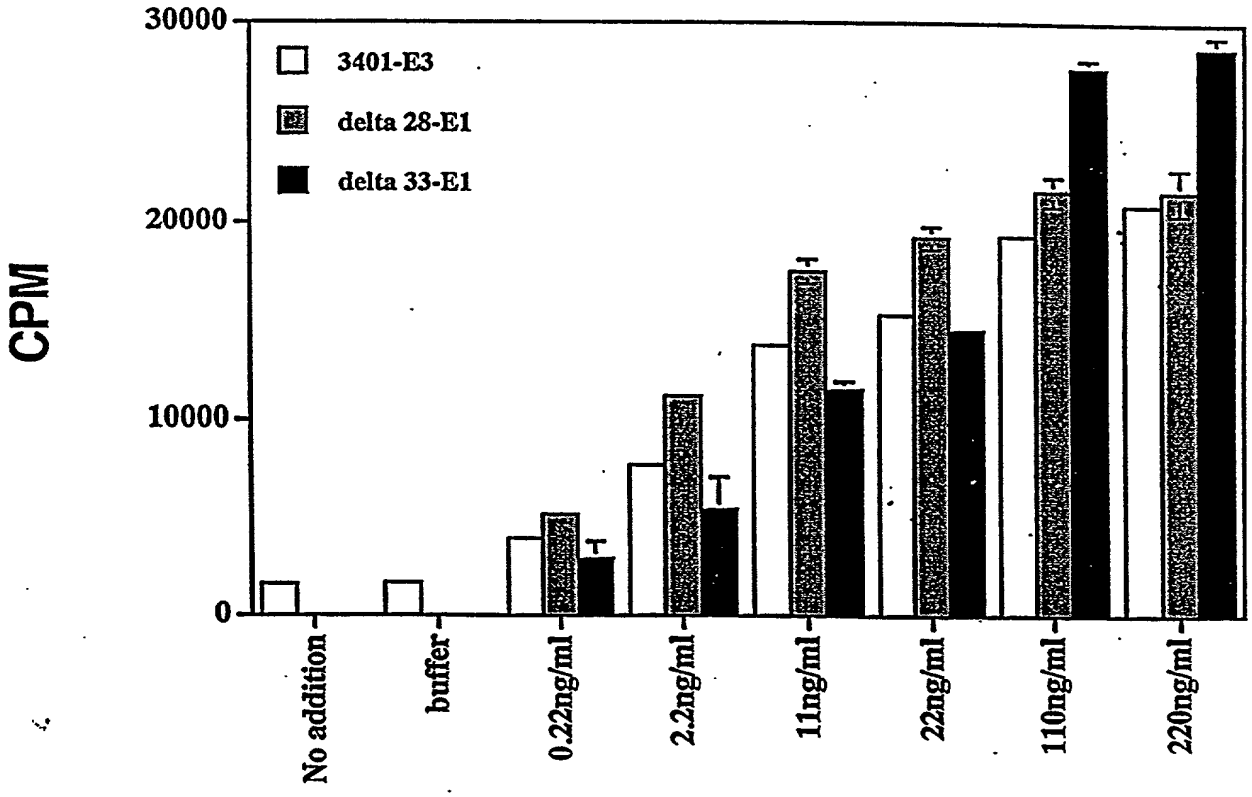

CPM
30000
20000
10000
0
3401-E3
delta 28-E1
delta 33-E1
No addition
buffer
0.22ng/ml
2.2ng/ml
11ng/ml
22ng/ml
110ng/ml
220ng/ml

Figure 23

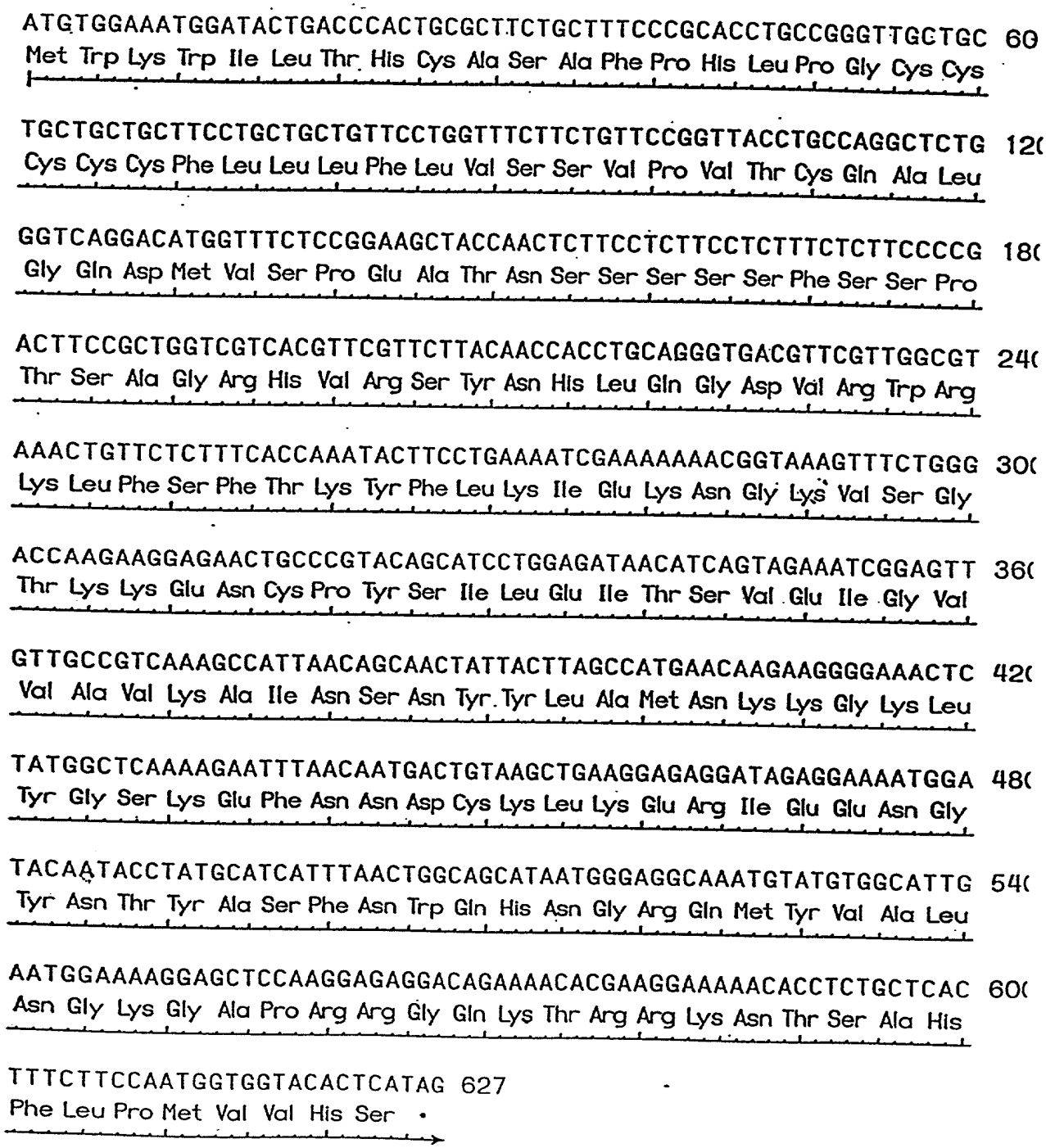

ATGTGGAAATGGATACTGACCCACTGCGCTTCTGCTTTCCCGCACCTGCCGGGTTGCTGC 60
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly Cys Cys
TGCTGCTGCTTCCTGCTGCTGTTCCTGGTTTCTTCTGTTCCGGTTACCTGCCAGGCTCTG 12(
Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val Pro Val Thr Cys Gln Ala Leu
GGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCCCG 18(
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro
ACTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT 24(
Thr Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCTGGG 30(
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly
ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 36(
Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val
GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC 42(
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu
TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 48(
Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG 54(
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu
AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC 60(
Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
TTTCTTCCAATGGTGGTACACTCATAG 627
Phe Leu Pro Met Val Val His Ser

Figure 24A

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT 60

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser

TCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAG 120

Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln

GGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA 180

Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys

AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA 240

Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr

TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATG 300

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met

AACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAG 360

Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu

AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420

Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg

CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG 480

Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg

AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG 525

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser •

Figure 24B

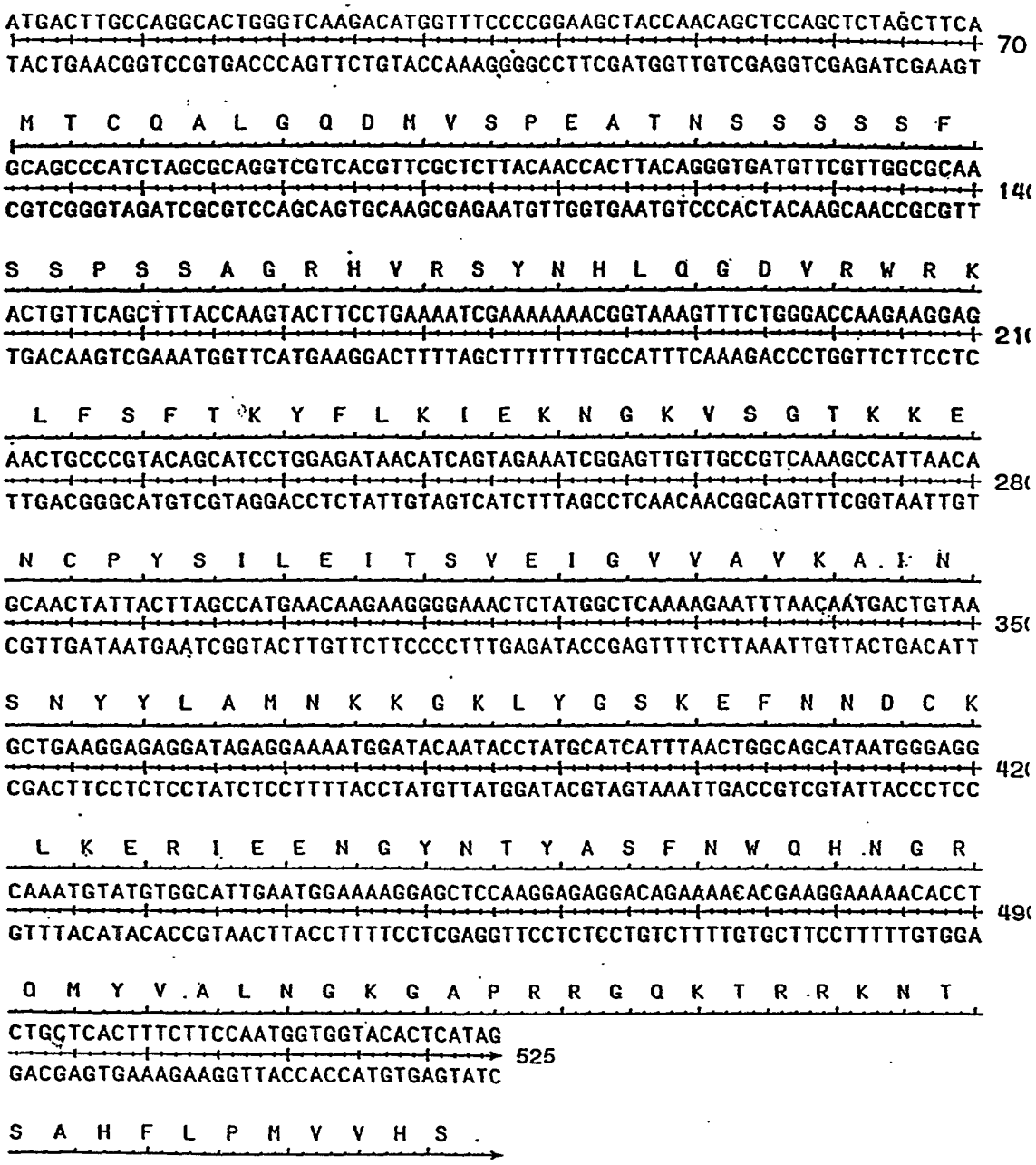

ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA
TACTGAACGGTCCGTGACCCAGTTCTGTACCAAAGGGGCCTTCGATGGTTGTCGAGGTCGAGATCGAAGT
70
M T C Q A L G Q D M V S P E A T N S S S S S F
GCAGCCCATCTAGCGCAGGTCGTCACGTTCGCTCTTACAACCACTTACAGGGTGATGTTCGTTGGCGCAA
CGTCGGGTAGATCGCGTCCAGCAGTGCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGCGTT
14(
S S P S S A G R H V R S Y N H L Q G D V R W R K
ACTGTTCAGCTTTACCAAGTACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAG
TGACAAGTCGAAATGGTTCATGAAGGACTTTTAGCTTTTTTTGCCATTTCAAAGACCCTGGTTCTTCCTC
21(
L F S F T K Y F L K I E K N G K V S G T K K E
AACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACA
TTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAACAACGGCAGTTTCGGTAATTGT
28(
N C P Y S I L E I T S V E I G V V A V K A I N
GCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAA
CGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAGATACCGAGTTTTCTTAAATTGTTACTGACATT
35(
S N Y Y L A M N K K G K L Y G S K E F N N D C K
GCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG
CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCC
42(
L K E R I E E N G Y N T Y A S F N W Q H N G R
CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCT
GTTTACATACACCGTAACTTACCTTTTCCTCGAGGTTCCTCTCCTGTCTTTTGTGCTTCCTTTTTGTGGA
49(
Q M Y V A L N G K G A P R R G Q K T R R K N T
CTGGTCACTTTCTTCCAATGGTGGTACACTCATAG
525
GACGAGTGAAAGAAGGTTACCACCATGTGAGTATC
S A H F L P M V V H S .

Figure 25

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCT
GCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAAT
CGAAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCC
TGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAA
TGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCAT
TTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCT
CCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAAT
GGTGGTACACTCATAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIE
KNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKL
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

Figure 26

ATGGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAAT
CGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAA
GGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGA
TAGAGGAAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG
CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACAC
GAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGV
VAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

Figure 27

ATGGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGAT
AACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTT
AGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTA
AGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGG
CAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAG
AGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTAC
ACTCATAG

MVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAM
NKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQ
KTRRKNTSAHFLPMVVHS.

Figure 28

ATGGAAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCAT
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCA
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAAC
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA
ATGGTGGTACACTCATAG

MEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDC
KLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH
S.

Figure 29

ATGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT
TGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC
TCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA
AATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTA
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAA
AACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGY
NTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

Figure 30

ATGGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACT
CTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAA
ATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATG
TGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAA
CACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

Figure 31

ATGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAG
GATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGA
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAAC
ACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT
RRKNTSAHFLPMVVHS.

Figure 32

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCT
GCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAAT
CGAAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCC
TGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAA
TGACTGTAAGCTGAAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIE
KNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKL
K

Figure 33

ATGGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAAT
CGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAA
GGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGV
VAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLK

Figure 34

C-37 To Ser

ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCT
GCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAAT
CGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCC
TGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAA
TGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCAT
TTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCT
CCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAAT
GGTGGTACACTCATAG

Figure 35

: C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCT
GCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAAT
CGAAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATCC
TGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAA
TGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCAT
TTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCT
CCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAAT
GGTGGTACACTCATAG

Figure 36

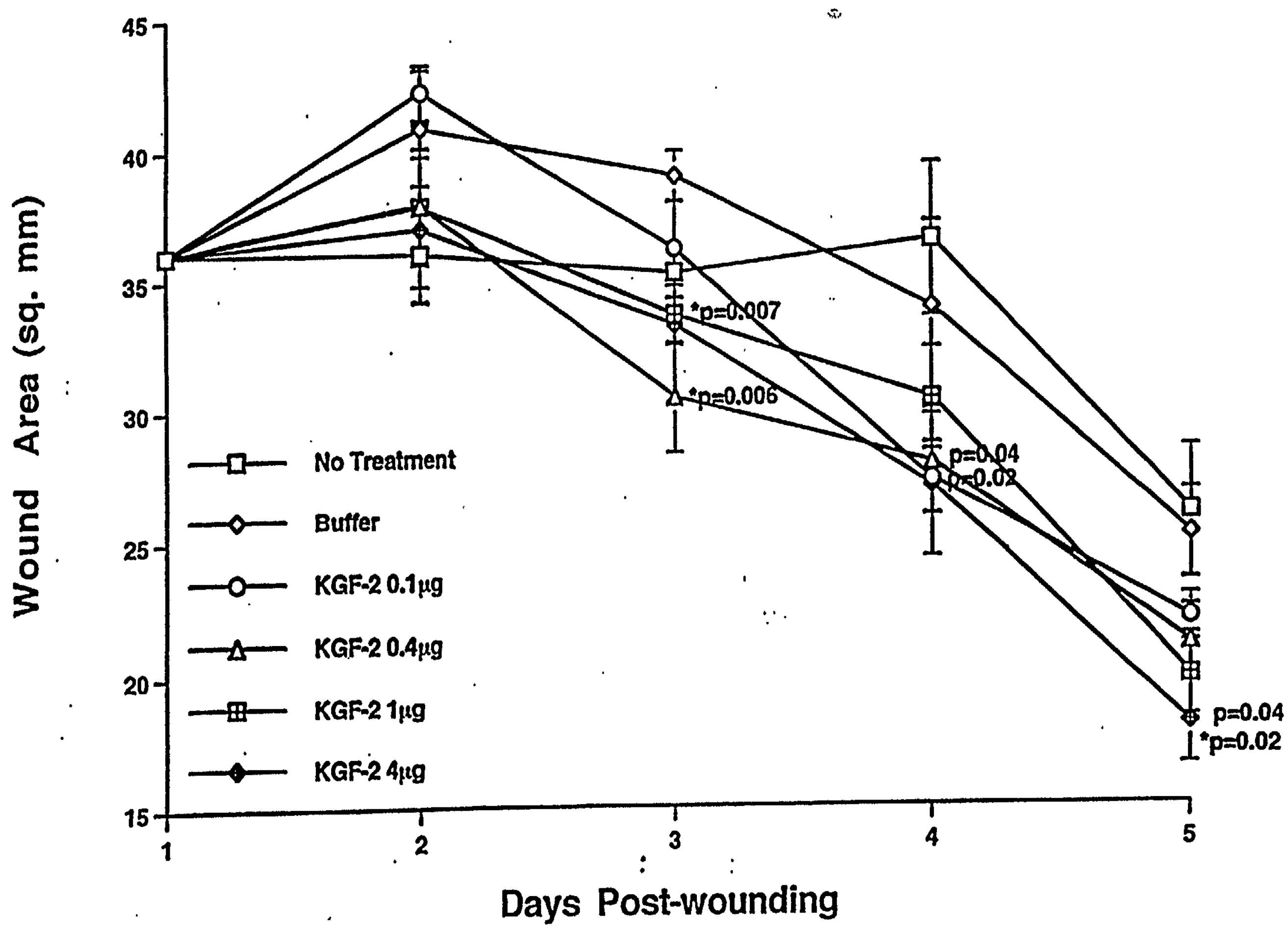


Figure 37

Effect of KGF-2 Δ33 on Normal Wound Healing Rat Model

Treatment Groups	Wound Size (mm)	%Wound Closure	Histological Score	Re-epith. (μm)	BrdU Score
No Treatment	25.9 ± 2.5	58.8 ± 3.7	6.8 ± 0.2	1142 ± 141	3.8 ± 0.4
Buffer	25.1 ± 1.7	60.2 ± 2.6	6.4 ± 0.2	923 ± 61	5.0 ± 0.4
KGF-2/Δ33 (0.1μg)	22.0 ± 0.9	65 ± 1.4	6.8 ± 0.2	1275 ± 148	4.6 ± 0.7
KGF-2/Δ33 (0.4 μg)	21.1 ± 1.4	68.4 ± 2.4	8.0 ± 0.5 p=0.0445*	1310 ± 182	4.2 ± 0.7
KGF-2/Δ33 (1.0μg)	19.9 ± 1.5	66.2 ± 2.1	8.4 ± 0.4 p=0.0159* p=0.0053†	1389 ± 115 p=0.0074†	3.3 ± 0.25 p=0.0217†
KGF-2/Δ33 (4.0μg)	18.1 ± 1.6 p=0.0398* p=0.0200†	71.2 ± 2.6 p=0.0367* p=0.0217†	8.5 ± 0.3 p=0.0047* p=0.0445†	1220 ± 89 p=0.0254†	5.3 ± 0.9

Figure 38

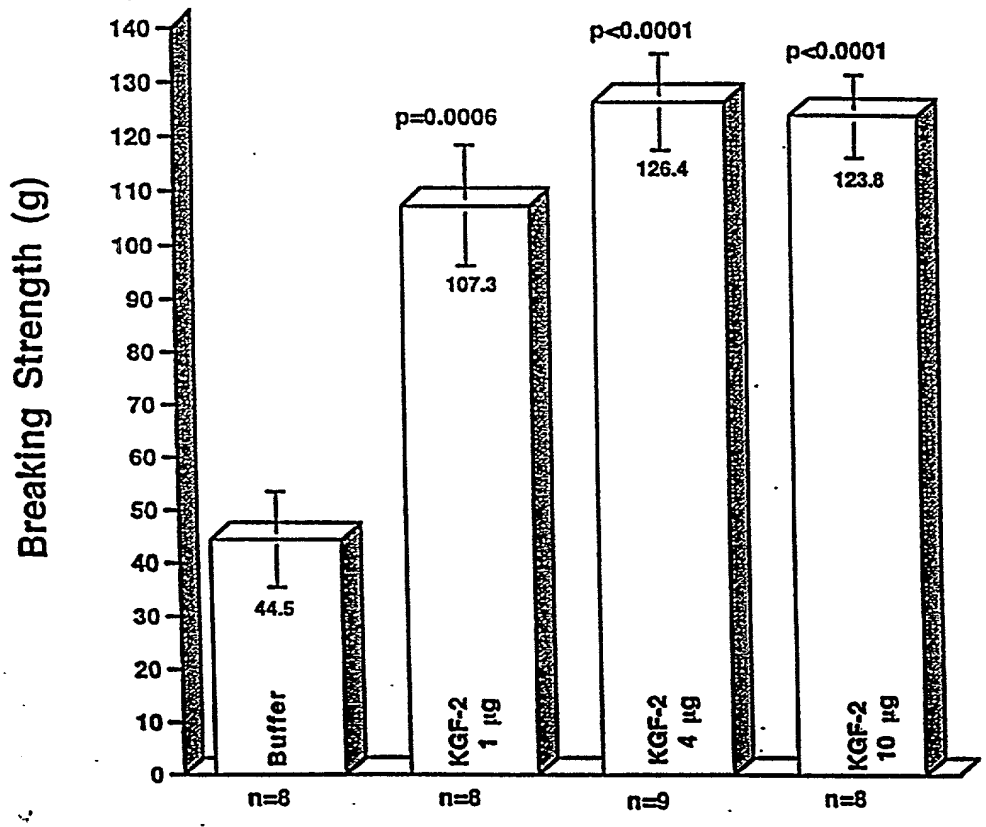

Breaking Strength (g)
140
130
120
110
100
90
80
70
60
50
40
30
20
10
0
44.5
107.3
126.4
123.8
p=0.0006
p<0.0001
p<0.0001
Buffer
KGF-2 1 µg
KGF-2 4 µg
KGF-2 10 µg
n=8
n=8
n=9
n=8

Figure 39

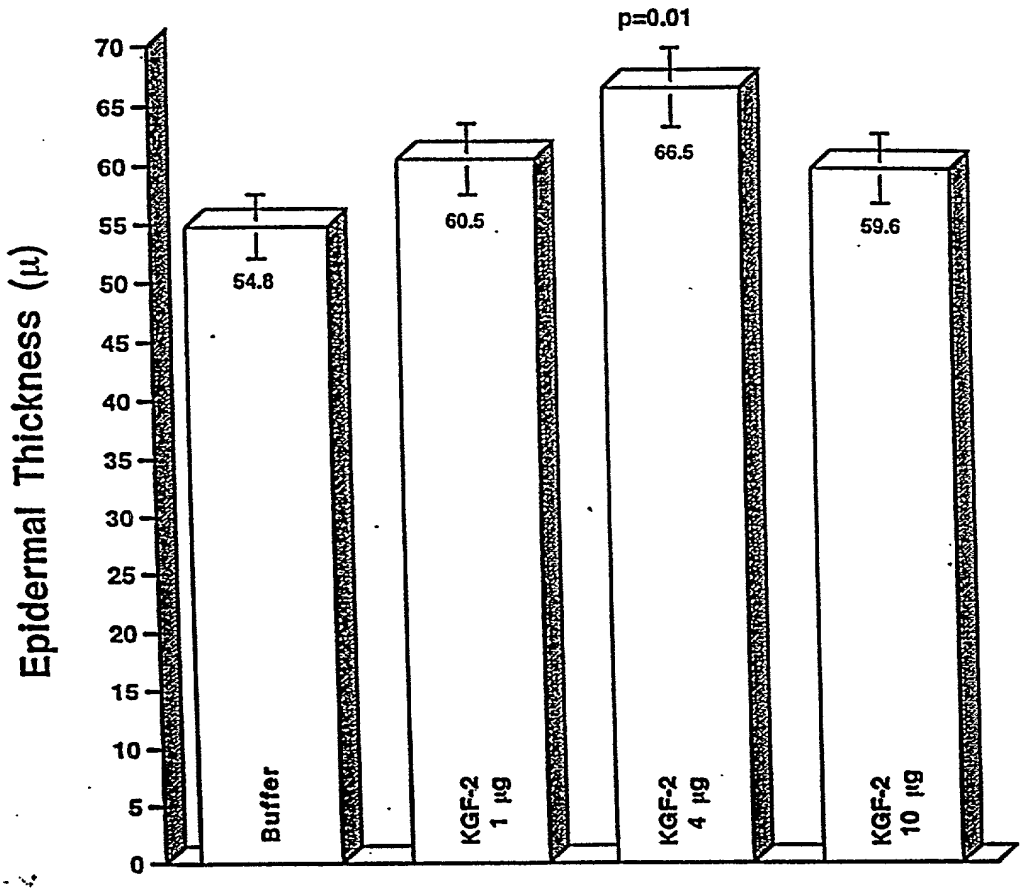

p=0.01
Epidermal Thickness (μ)
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
54.8
60.5
66.5
59.6
Buffer
KGF-2 1 μg
KGF-2 4 μg
KGF-2 10 μg

Figure 40

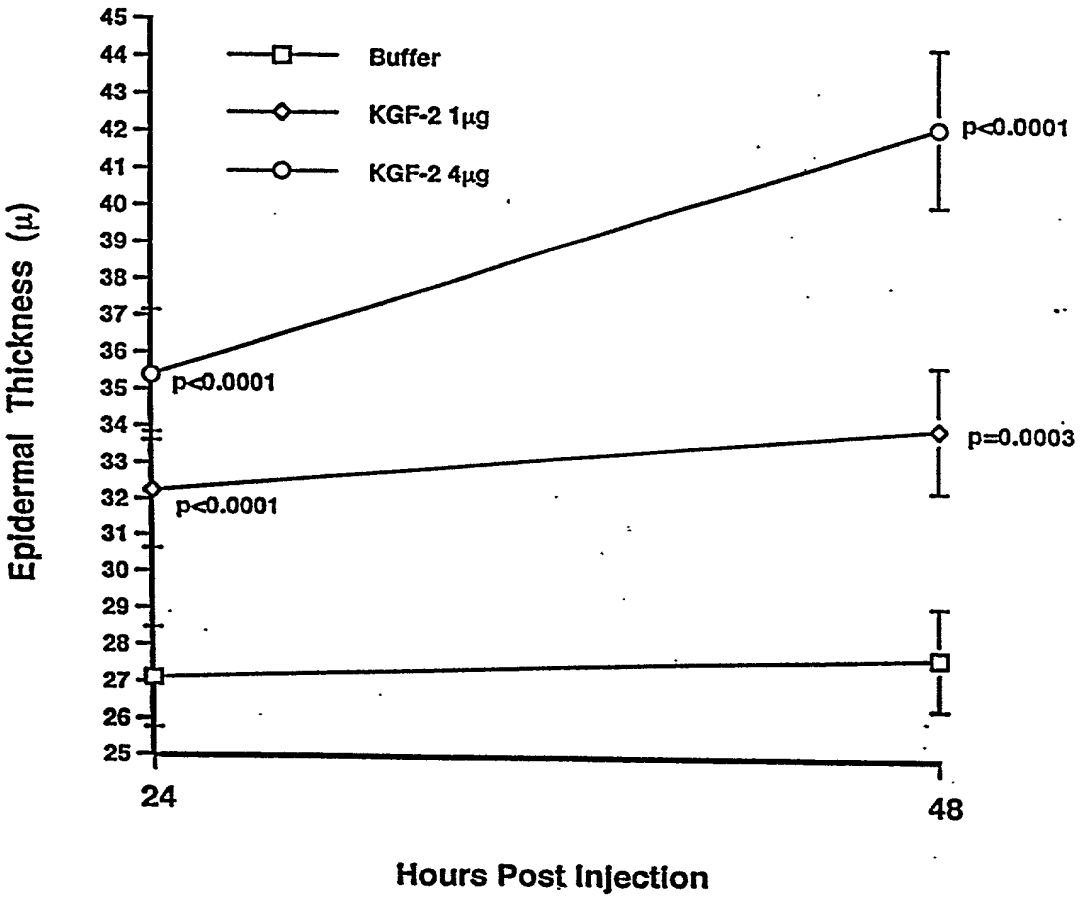

Buffer
KGF-2 1µg
KGF-2 4µg
p<0.0001
p<0.0001
p=0.0003
Epidermal Thickness (µ)
45
44
43
42
41
40
39
38
37
36
35
34
33
32
31
30
29
28
27
26
25
24
48
Hours Post Injection

Figure 41

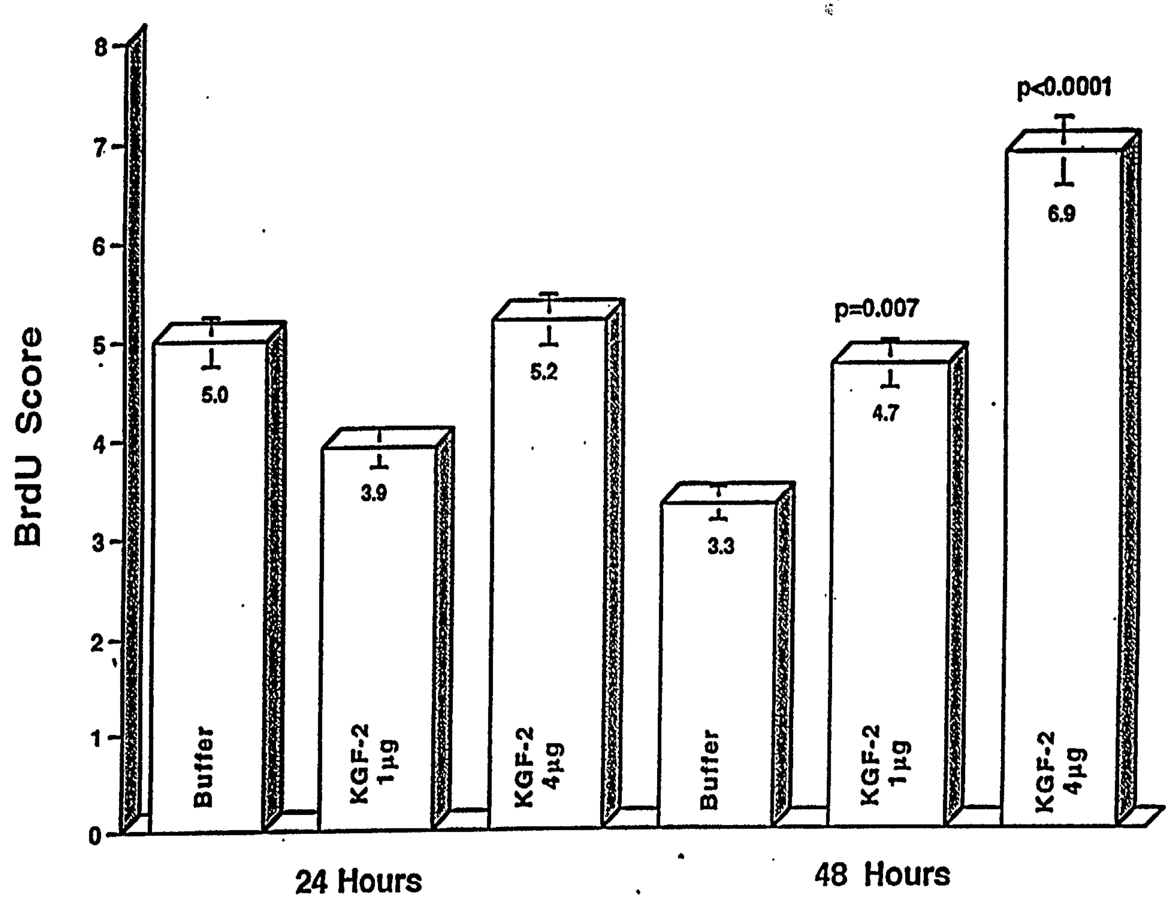
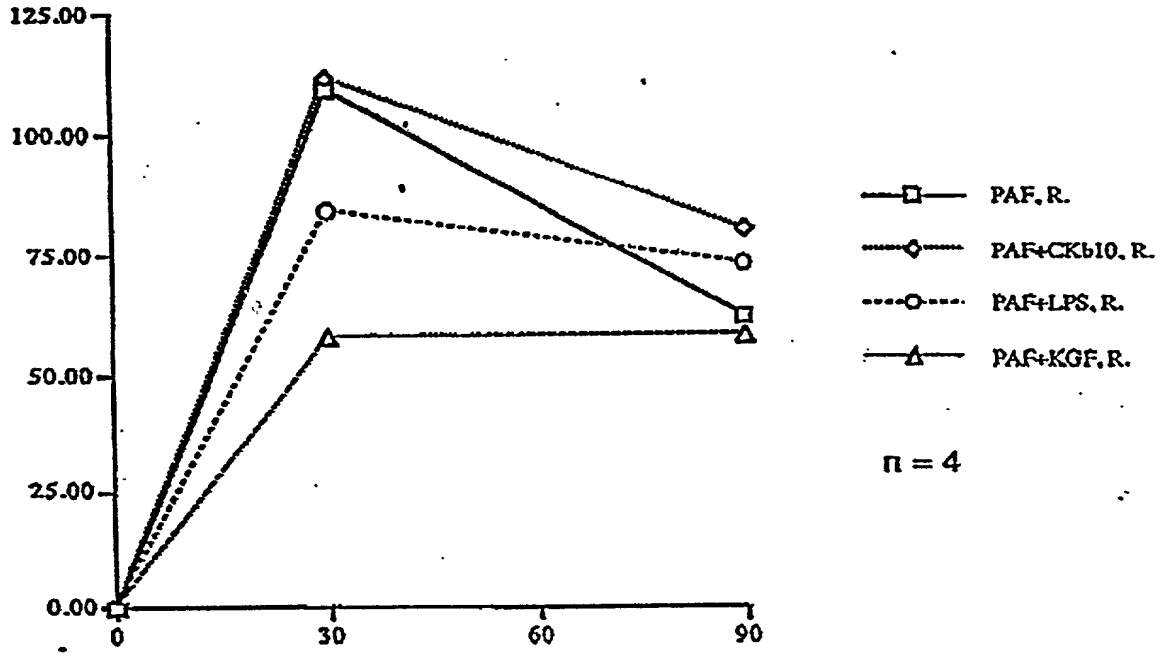
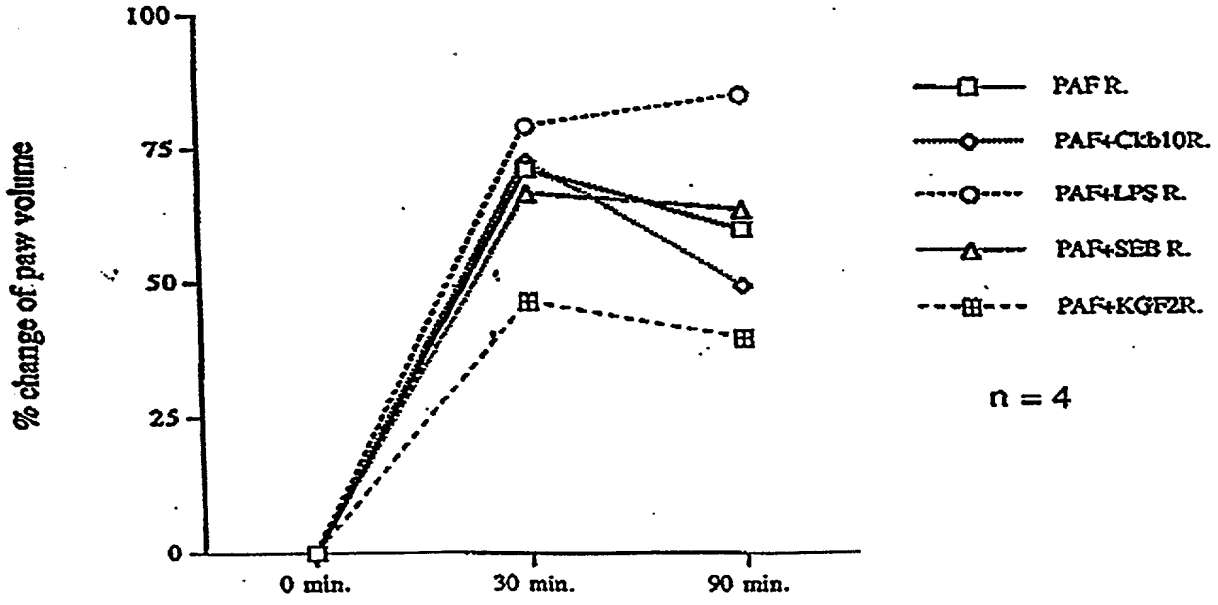

BrdU Score
0
1
2
3
4
5
6
7
8
5.0
3.9
5.2
3.3
4.7
6.9
p=0.007
p<0.0001
Buffer
KGF-2 1µg
KGF-2 4µg
Buffer
KGF-2 1µg
KGF-2 4µg
24 Hours
48 Hours

Figure 42

No.1



No.2



Minutes post injection

Effect of KGF-2 Δ33 on PAF-induced paw edema in Lewis rats

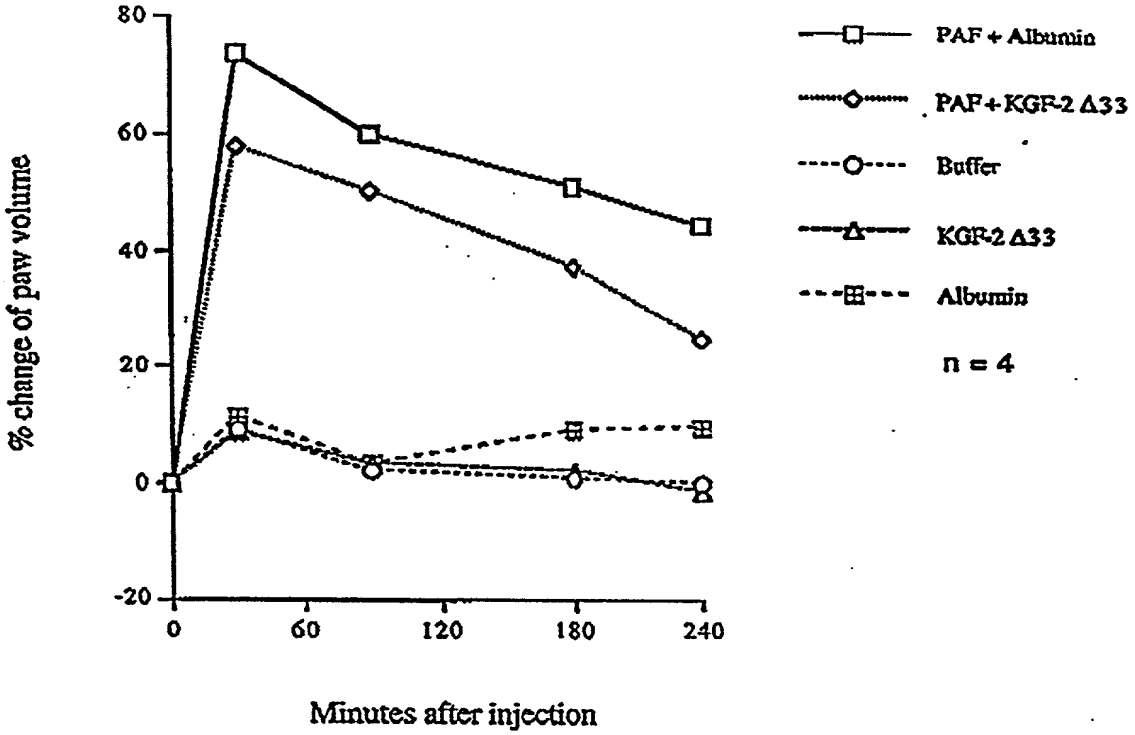


Figure 43

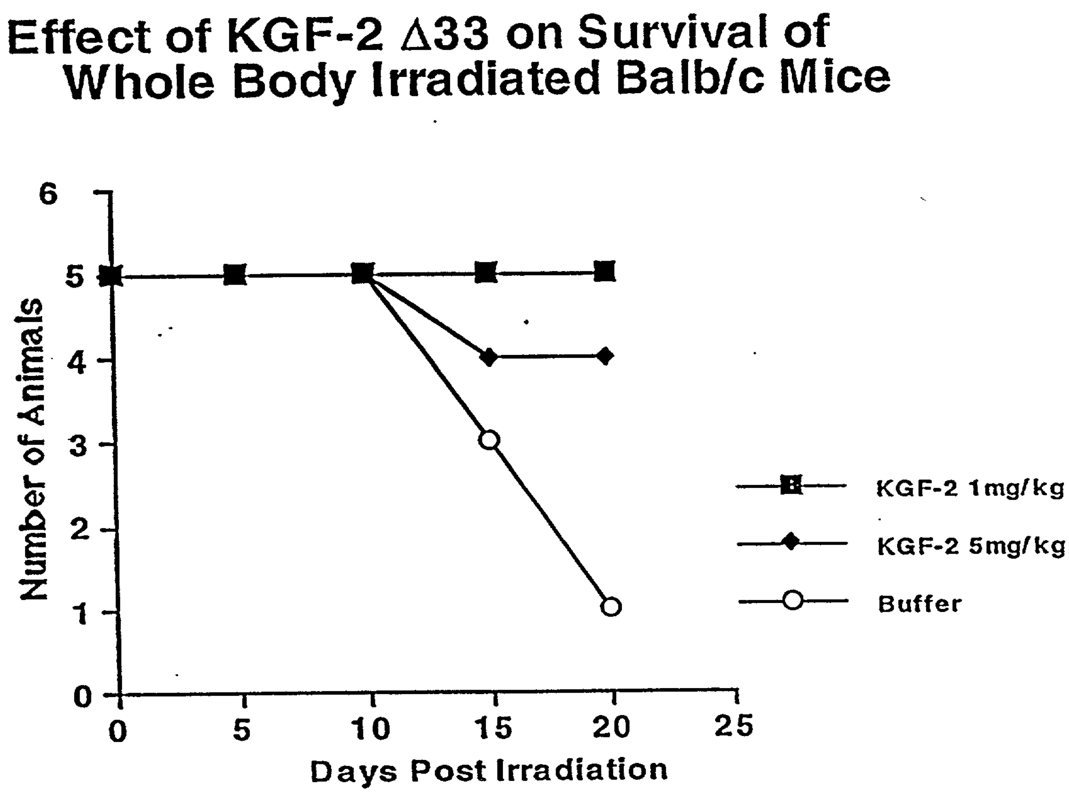

Effect of KGF-2 Δ33 on Survival of Whole Body Irradiated Balb/c Mice
Number of Animals
6
5
4
3
2
1
0
0
5
10
15
20
25
Days Post Irradiation
KGF-2 1mg/kg
KGF-2 5mg/kg
Buffer

Figure 44

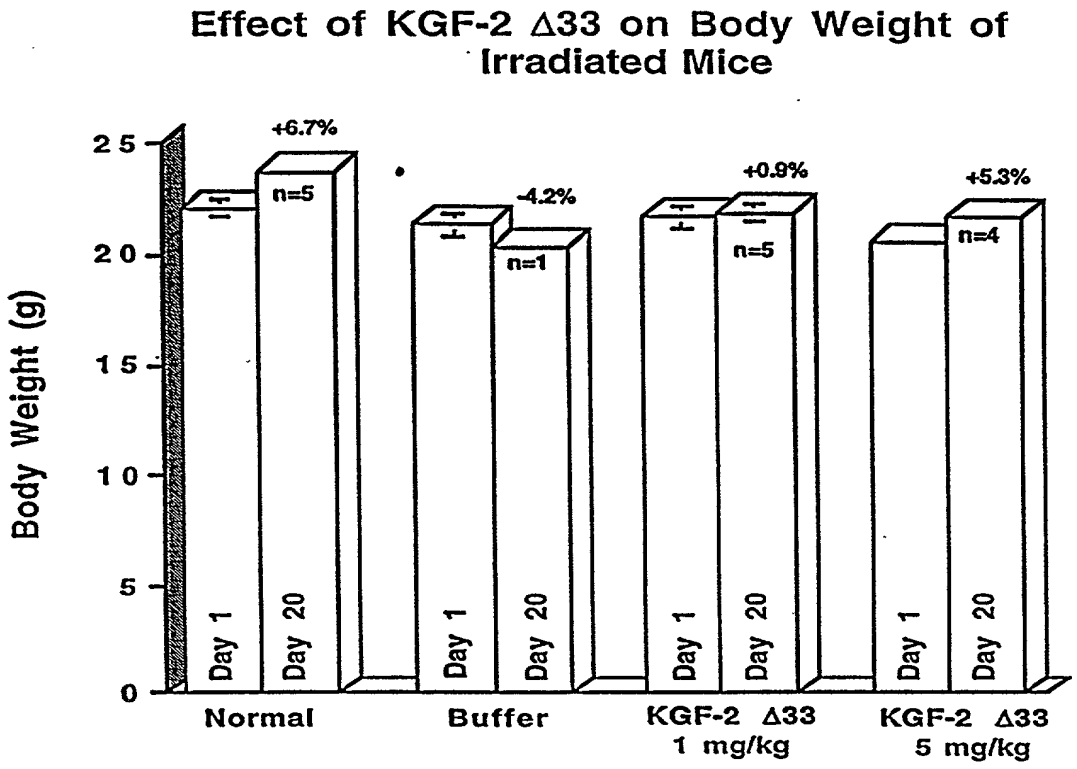

Effect of KGF-2 Δ33 on Body Weight of Irradiated Mice
Body Weight (g)
25
20
15
10
5
0
+6.7%
n=5
-4.2%
n=1
+0.9%
n=5
+5.3%
n=4
Day 1
Day 20
Normal
Buffer
KGF-2 Δ33 1 mg/kg
KGF-2 Δ33 5 mg/kg

Figure 45

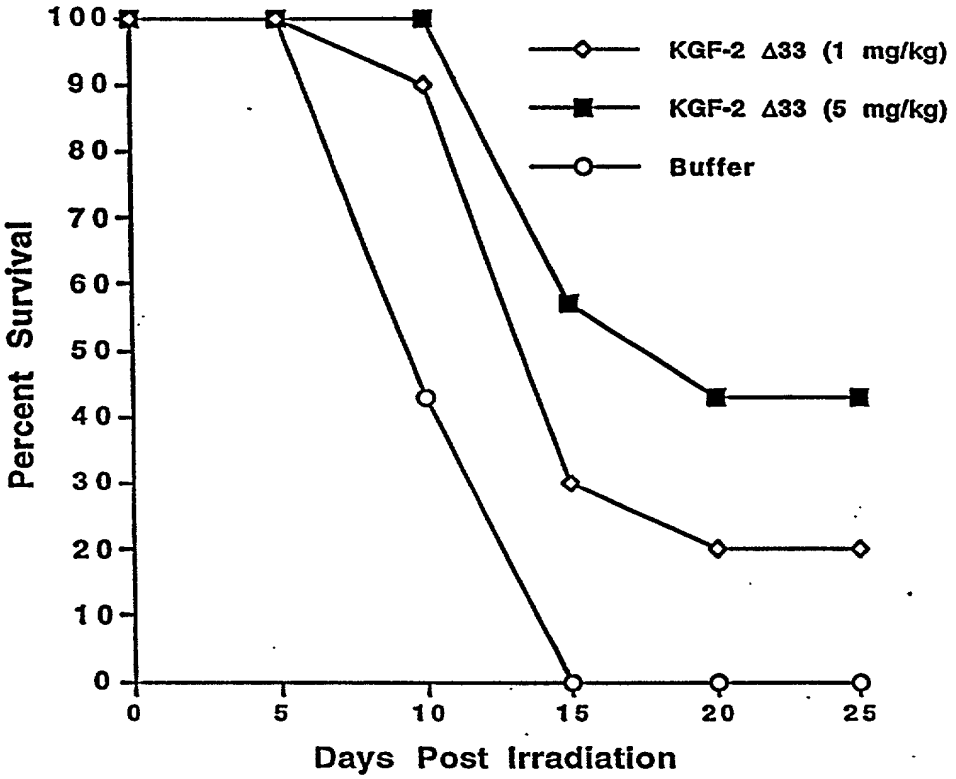

100
90
80
70
60
50
40
30
20
10
0
Percent Survival
0
5
10
15
20
25
Days Post Irradiation
KGF-2 Δ33 (1 mg/kg)
KGF-2 Δ33 (5 mg/kg)
Buffer

Figure 46

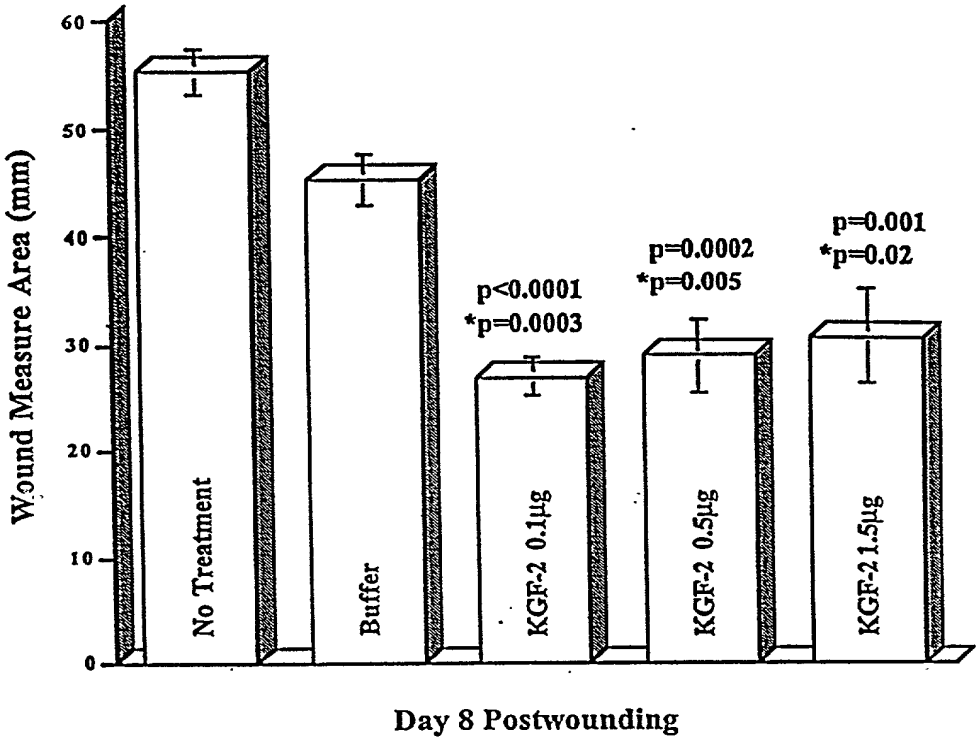
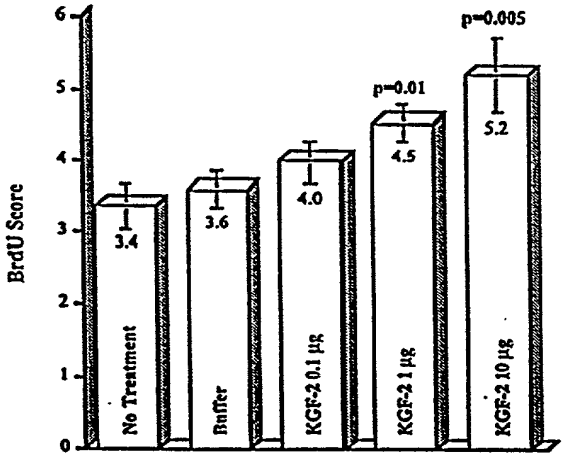

Wound Measure Area (mm)
60
50
40
30
20
10
0
No Treatment
Buffer
p<0.0001
*p=0.0003
KGF-2 0.1µg
p=0.0002
*p=0.005
KGF-2 0.5µg
p=0.001
*p=0.02
KGF-2 1.5µg
Day 8 Postwounding

Figure 47

Figure 48


BrdU Score
0
1
2
3
4
5
6
3.4
3.6
4.0
4.5
5.2
p=0.01
p=0.005
No Treatment
Buffer
KGF-2 0.1 µg
KGF-2 1 µg
KGF-2 10 µg

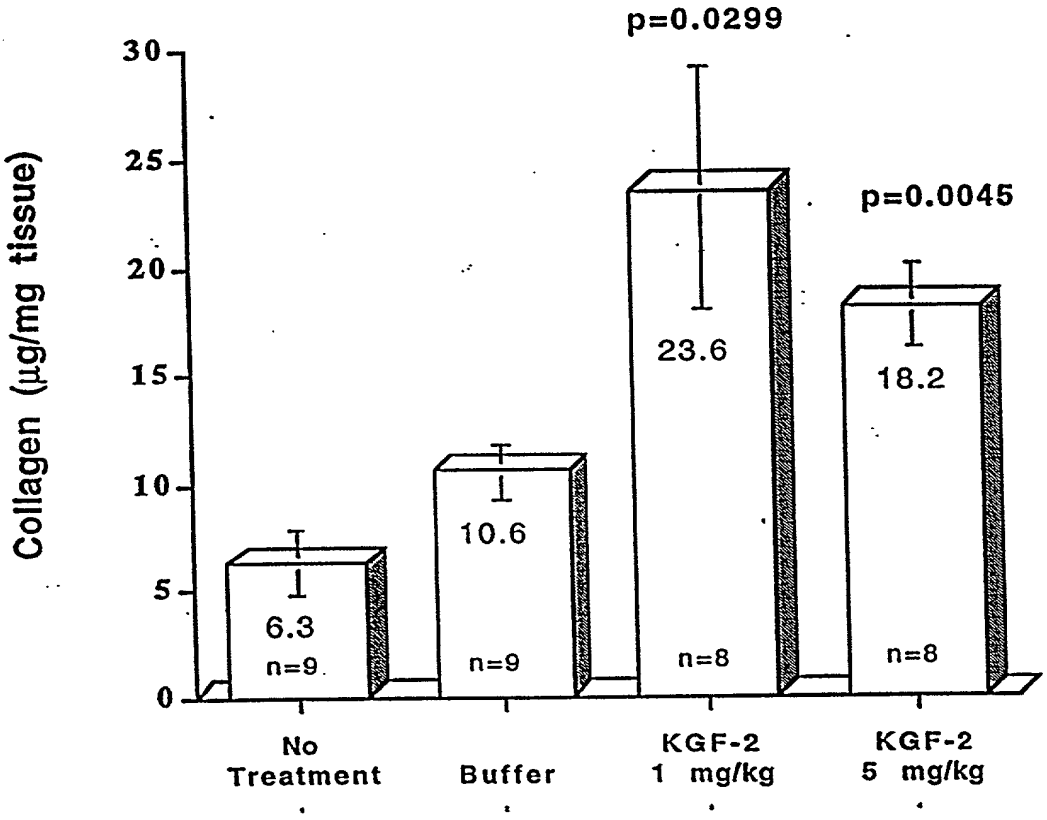

p=0.0299
p=0.0045
Collagen (µg/mg tissue)
30
25
20
15
10
5
0
6.3
n=9
10.6
n=9
23.6
n=8
18.2
n=8
No Treatment
Buffer
KGF-2 1 mg/kg
KGF-2 5 mg/kg

Figure 49

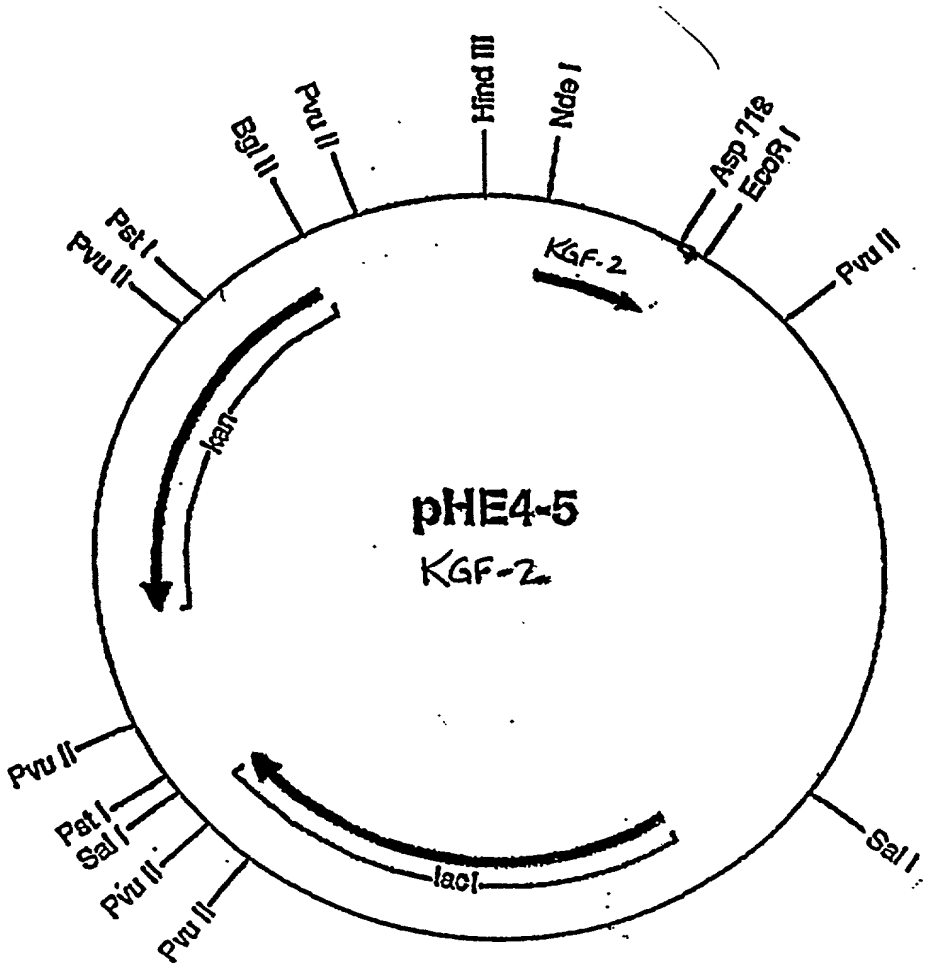

Hind III
Nde I
Asp 718
EcoR I
Pvu II
Bgl II
Pvu II
Pst I
Pvu II
KGF-2
Pvu II
kan
pHE4-5
KGF-2
Pvu II
Pst I
Sal I
Pvu II
Pvu II
lacI
Sal I

FIGURE 50

FIGURE 51

1	*AAGCTT* AAAAAACTGCAAAAAATAGT **[TTGACT]** (-35) TGTGAGCGGATAACAAT (Operator 1)	
50	**[TAAGAT]** (-10) GTACCCA ATTGTGAGCGGATAACAAT (Operator 2) TTCACACATTAA	
94	A **[GAGGAG]** (S/D) AAATTA *CATATG*	

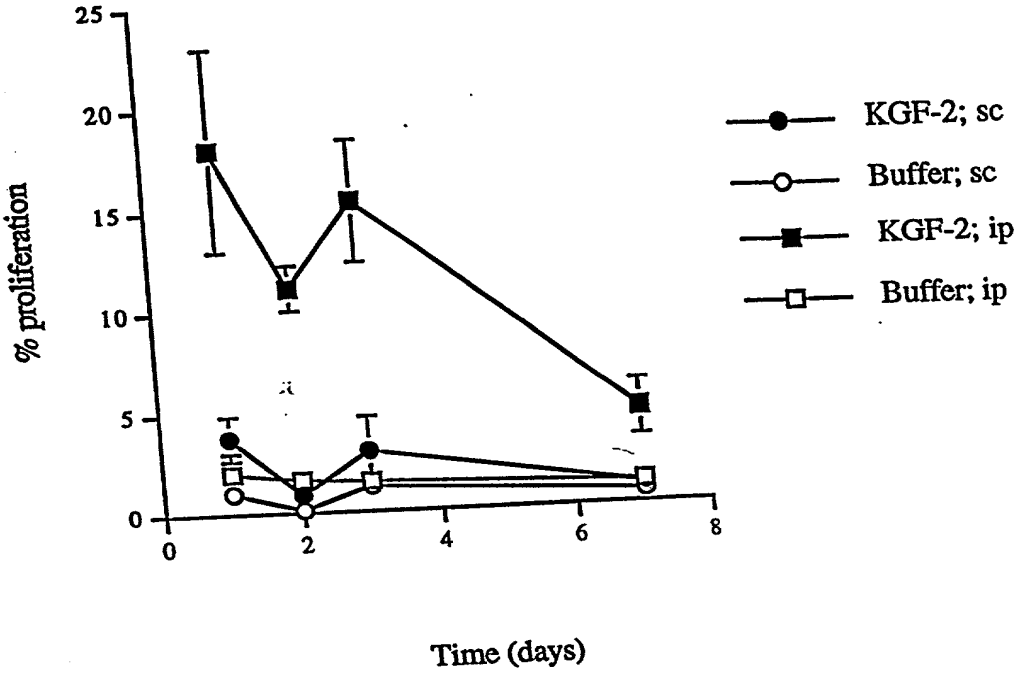

25
20
15
10
5
0
% proliferation
0
2
4
6
8
Time (days)
KGF-2; sc
Buffer; sc
KGF-2; ip
Buffer; ip

FIGURE 52

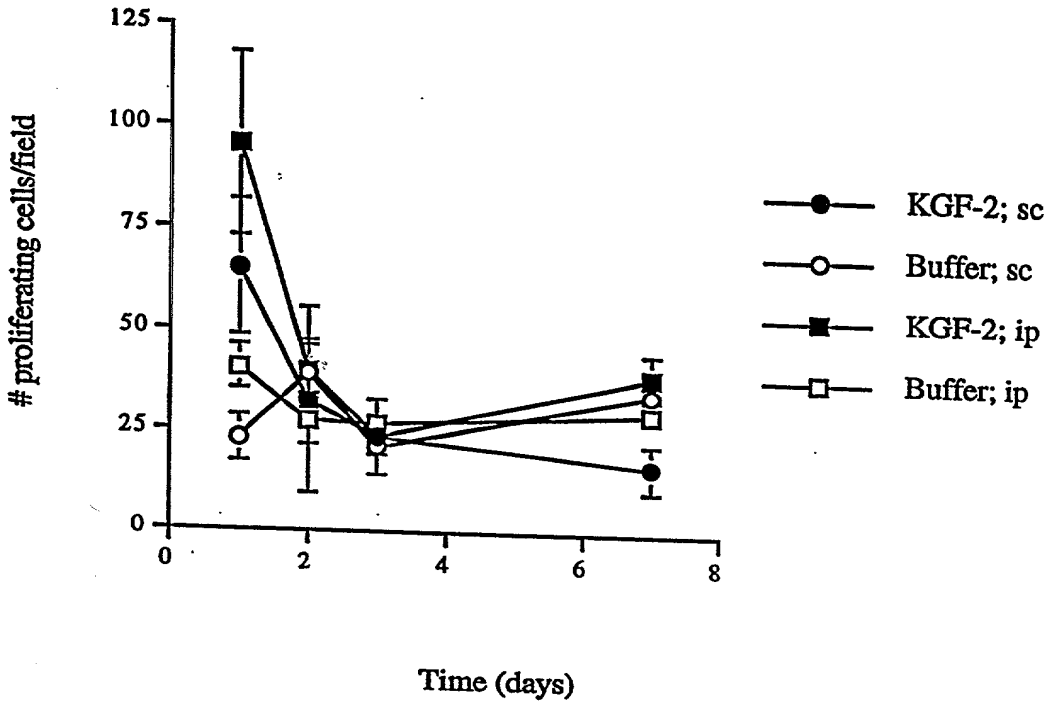

125
100
75
50
25
0
0
2
4
6
8
proliferating cells/field
Time (days)
KGF-2; sc
Buffer; sc
KGF-2; ip
Buffer; ip

FIGURE 53

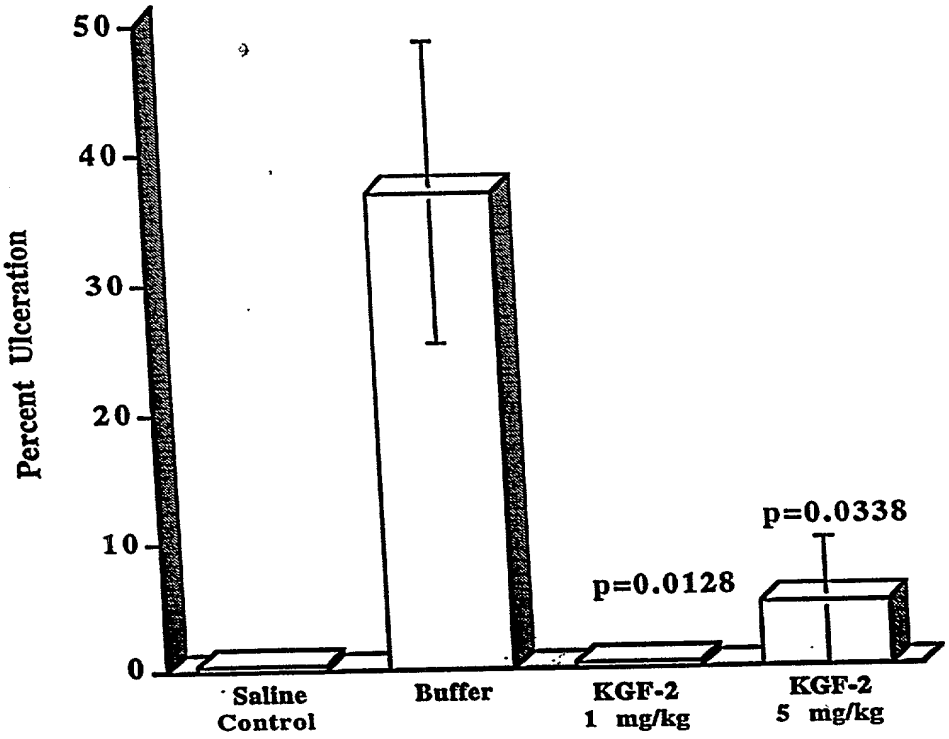


FIGURE 54

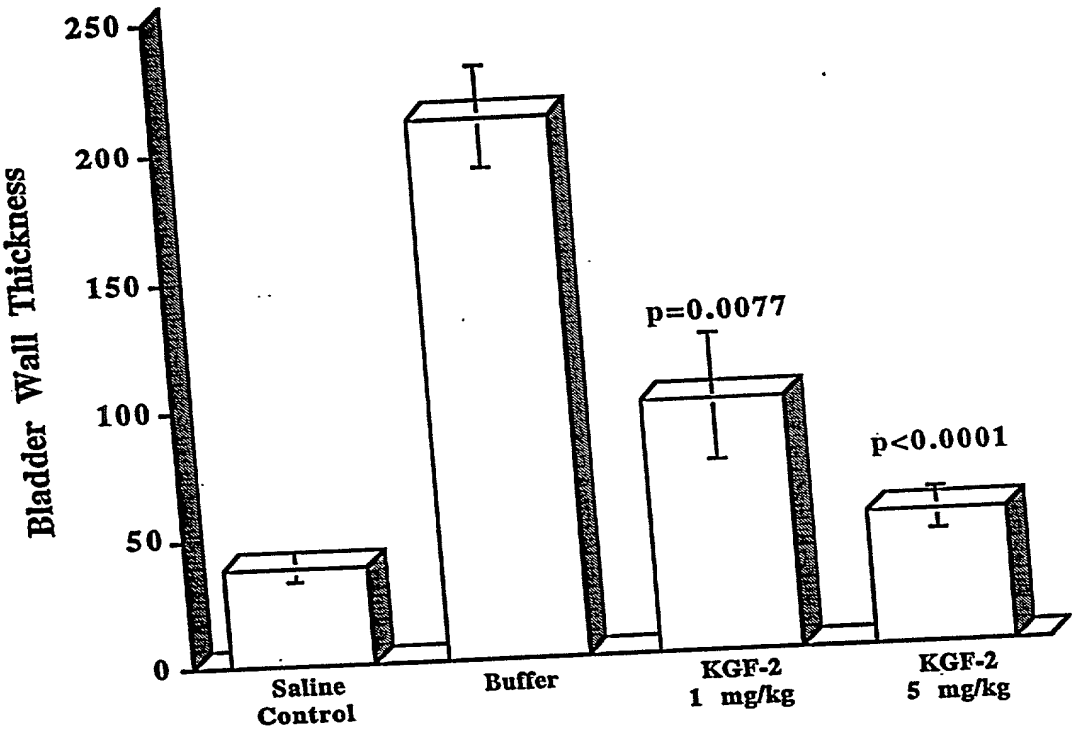

Bladder Wall Thickness
250
200
150
100
50
0
p=0.0077
p<0.0001
Saline Control
Buffer
KGF-2 1 mg/kg
KGF-2 5 mg/kg

FIGURE 55

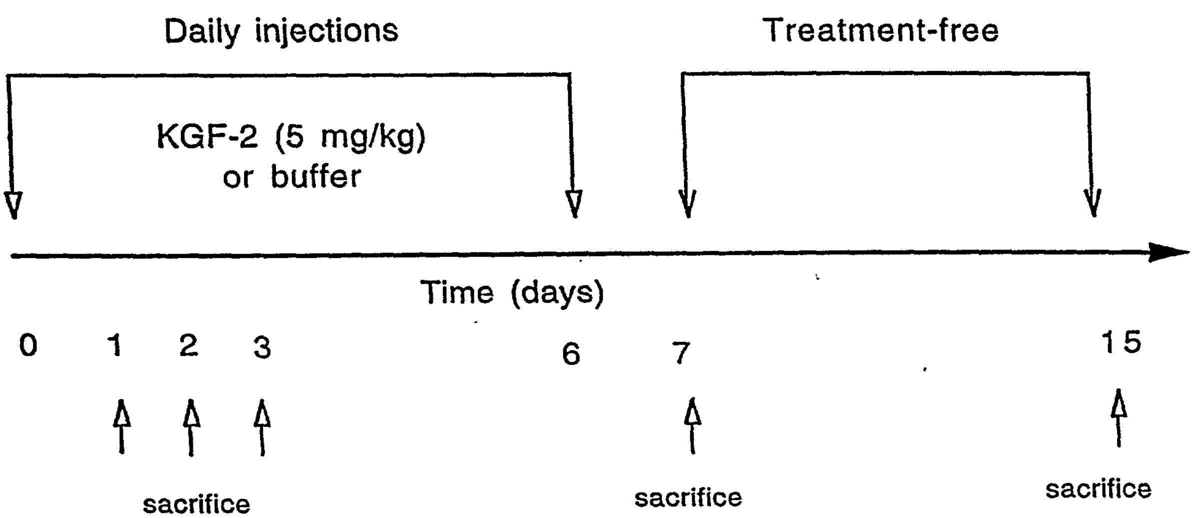

Daily injections
Treatment-free
KGF-2 (5 mg/kg)
or buffer
Time (days)
0
1
2
3
6
7
15
sacrifice
sacrifice
sacrifice

FIGURE 56

Proliferation of hepatocytes following systemic administration of KGF-2

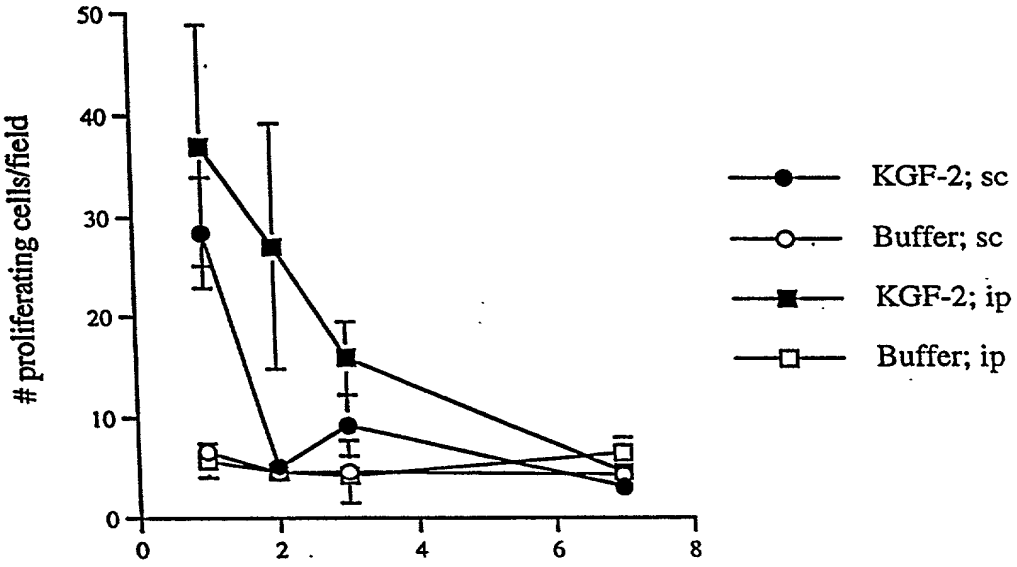


FIGURE 57

Proliferation of pancreatic cells following systemic administration of KGF-2

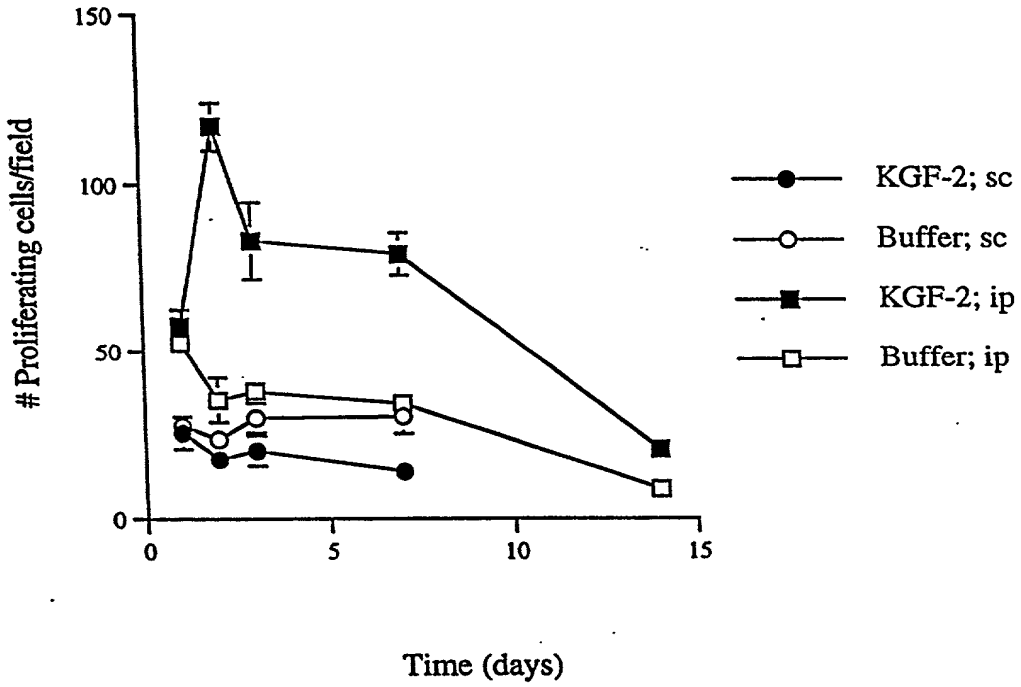


FIGURE 58

Proliferation of renal epithelia after systemic administration of KGF-2

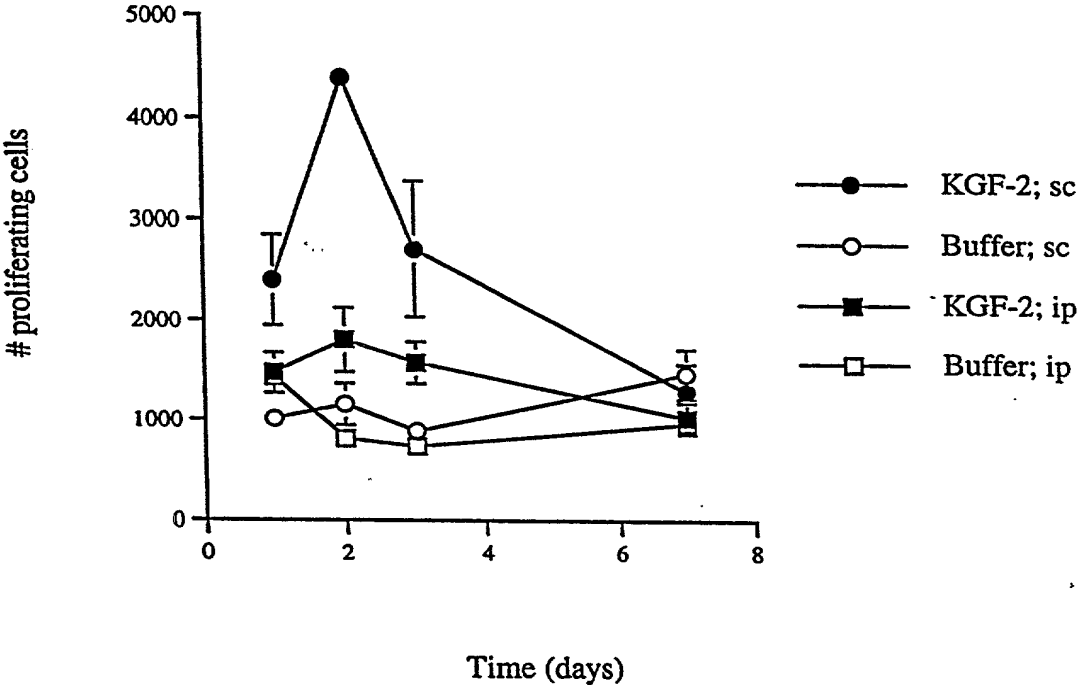


FIGURE 59

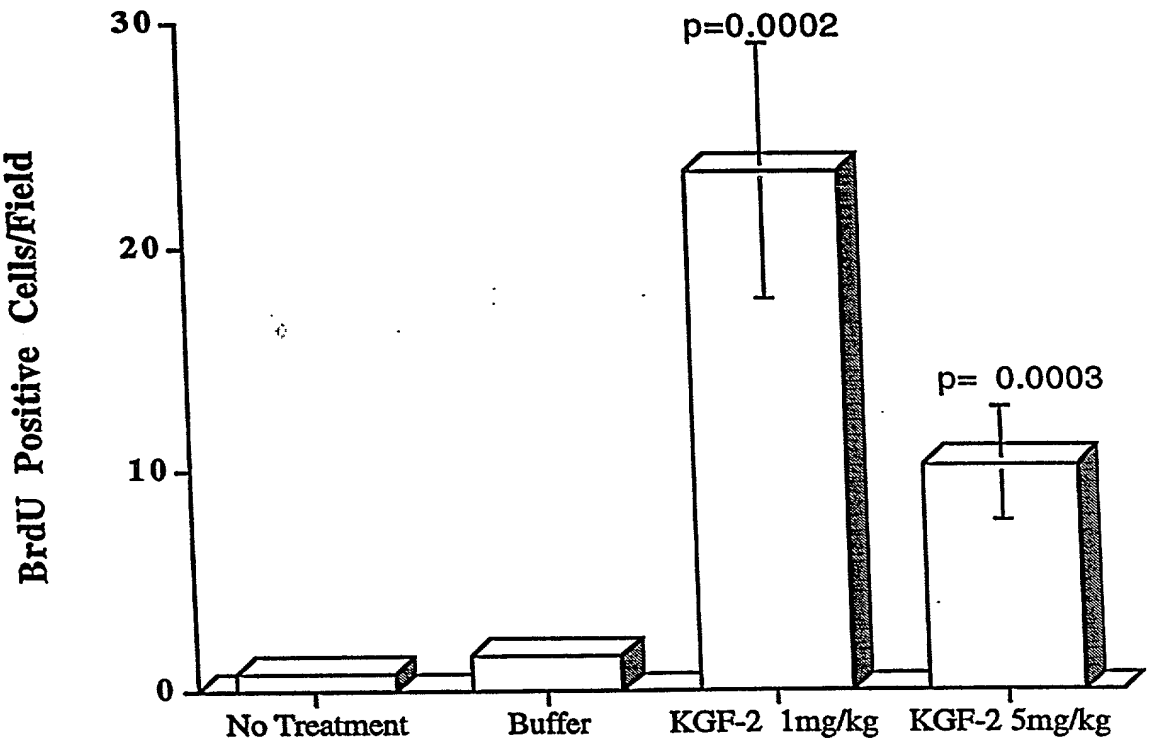

30
20
10
0
BrdU Positive Cells/Field
p=0.0002
p= 0.0003
No Treatment
Buffer
KGF-2 1mg/kg
KGF-2 5mg/kg

FIGURE 60